

SEARCH REQUEST FORM

12-366

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Art Unit: _____

7E09

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 12-10-98
Searcher: POB x8-4291
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CPU time: _____
Total time: _____
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Number of Databases: 6

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Type of Search

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1 A.A. Sequence
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____ STN
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____ DARC/Questel
MP3 Other

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(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:15:56 1998; MasPar time 27.66 Seconds
Tabular output not generated. 547.553 Million cell updates/sec

Title: >US-08-455-970-12
Description: (1-936) from US08455970. pep
Perfect Score: 6217
Sequence: 1 MATVIDUSFPKTKAKIILY.....LSSIQFARGSHWSYGLRPG 936

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-genes32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 37.888; Variance 222.402; scale 0.170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6217	100.0	977	19	LKT-GnRH protein fusi	0.00e+00
2	6193	99.6	936	7	GnRH-leukotoxin gene	0.00e+00
3	6135	98.7	1069	9	Bovine IFNgamma/LKT c	0.00e+00
4	6135	98.7	1069	21	Chimeric protein #2.	0.00e+00
5	6128	98.6	926	3	LKT352	0.00e+00
6	6128	98.6	926	7	Leukotoxin 352 produc	0.00e+00
7	6128	98.6	926	10	Recombinant leukotoxi	0.00e+00
8	6117	98.4	924	8	Recombinant leukotoxi	0.00e+00
9	6117	98.4	924	8	Recombinant leukotoxi	0.00e+00
10	6117	98.4	924	8	Recombinant leukotoxi	0.00e+00
11	6119	98.4	925	19	P. haemolytica trunca	0.00e+00
12	6107	98.2	943	7	Somatostatin-leukotox	0.00e+00
13	6100	98.1	951	7	Rotavirus VP4-leukoto	0.00e+00
14	6094	98.0	924	3	Leukotoxin 352 encode	0.00e+00
15	6057	97.4	1098	21	Chimeric protein #1.	0.00e+00
16	6050	97.3	1098	4	Bovine IL-2 - LKT fus	0.00e+00
17	6047	97.3	1098	9	Bovine IL-2/LKT chime	0.00e+00
18	6046	97.2	953	8	Leukotoxin protein.	0.00e+00

19	6037	97.1	953	2	R07167	105KD PTX protein of	0.00e+00
20	6037	97.1	953	11	R60072	PtxA protein of Paste	0.00e+00
21	6022	96.9	953	3	R15159	Leukotoxin from P. ha	0.00e+00
22	4925	79.2	934	20	W07637	P. suis leukotoxin ge	0.00e+00
23	4254	68.4	956	25	W22156	Apxiic protein.	3.65e-297
24	4254	68.4	956	3	R12561	APPA haemolysin anti	3.65e-297
25	2566	41.3	1049	25	W22159	ApxiIIB protein.	1.80e-173
26	2566	41.3	1244	10	R54781	Leukotoxin AppliIA.	1.80e-173
27	2291	36.9	1022	25	W22152	ApxiA protein.	2.16e-153
28	2244	35.8	1023	15	R76991	LhaA (low homology to	5.80e-150
29	2223	35.8	544	19	W03943	LKT-GnRH protein fusi	1.97e-148
30	2167	34.9	1334	10	R50290	lktA::lacZ fusion pro	2.39e-144
31	2160	34.7	1334	3	R14481	lktA::lacZ fusion prod	2.72e-144
32	2056	33.1	1403	3	R10890	lktA::lacZ fusion pro	2.92e-136
33	1758	28.3	758	17	R85998	Enterohaemorrhagic E.	1.39e-114
34	893	14.4	1522	2	P93357	Sequence of the catal	3.51e-52
35	896	14.4	1705	2	P94365	Sequence of part of a	2.14e-52
36	893	14.4	1706	2	R08031	Adenyl cyclase from B	3.51e-52
37	885	14.2	1445	2	R12108	N-terminal deleted ad	1.31e-51
38	433	7.3	1263	25	W13503	B. pertussis adenylcy	3.22e-21
39	448	7.2	1262	25	W13505	B. bronchiseptica ade	7.10e-21
40	440	7.1	1644	25	W13504	B. bronchiseptica ade	2.52e-20
41	443	7.1	1645	25	W13502	B. pertussis adenylcy	1.57e-20
42	281	4.5	127	15	R76990	Actinobacillus antige	1.32e-09
43	276	4.4	900	4	R20568	Sequence of a partial	2.82e-09
44	223	3.6	997	10	R54630	Mannuronan C-5-epimer	7.57e-06
45	215	3.5	617	24	W27247	Pseudomonas fluoresce	2.44e-05

ALIGNMENTS

RESULT 1
ID W03942 standard; Protein; 977 AA.

AC W03942;
DT 20-NOV-1996 (first entry)
DE LKT-GnRH protein fusion from pCB113.
KW Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;
KW fusion protein; immunogen; vaccine; fertility control;
KW contraceptive; sterilisation.
OS Chimeric Pasteurella haemolytica A1 strain B122;
ES Chimeric synthetic.
FH Key Location/Qualifiers
FT domain 1..929
FT /label= LKT
FT domain 927..977
FT /label= GnRH_repeat_domain
FT W0624675-A1.
PN 15-AUG-1996
PD 24-JAN-1996; CA0049.
PR 10-FEB-1995; US-387156.
PA (UYSA-) UNIV SASKATCHEWAN.
PI Manns JG, Potter AA;
DR WPI: 96-384447/38.
DR N-PSDB: T37176.
PT Gonadotropin-releasing hormone multimer fusion proteins - with
PT leukotoxin polypeptide for increased immunogenicity, useful in
PT antifertility vaccine prodn.
PS Claim 7; Fig 5A-5H; 87pp; English.
CC A chimeric protein (W03942) is composed of a fusion between
CC also W03945) and a 4-copy gonadoliberin-releasing hormone (GnRH)
CC repeat sequence (see also W03944). It is the product of a
CC chimeric gene (T37176) produced by ligating a synthetic sequence
CC for the 4-copy GnRH into vector pAA352 (ATCC 68283), which carries
CC the LKT-352 gene. Recombinant plasmid pCB113 (LKT 352.4 copy
CC GnRH, ATCC 69749) was obt'd. Escherichia coli transformants
CC produced the chimeric protein, which is useful as a vaccine for
CC fertility control, esp. immunological sterilisation of
CC domestic or farm animals.
SQ Sequence 977 AA;

Query Match 100.0%; Score 6217; DB 19; Length 977;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;

	Matches	936:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
Db	1	matvidlsfpktgakkililvipqnydydteqngldlvkaaeelgievqreennia	60							
Qy	1	MATVIDLSFPKTKGAKKILILIPQNYDYDTEQNGLDLVKAAEELGIEVQREENNIA	60							
Db	61	qtslgtiqtaiqltergvlvsapqldklqktkagaglsaesivqnanakvlgsgigs	120							
Qy	61	QTSLGTIQTAIQLTERGIVLSAPOIDKLLQKTKAGAGLSAESIVQNAKAKTVLSGIGS	120							
Db	121	ilgsvlagmdildealqnnqnalakagieltnslteniansvktldetfgeqisqfsgkl	180							
Qy	121	ILGSVLAGMDILDEALQNNQNALAKAGIELTNSLTENIANSVKTLDETFGEQISQFSGKL	180							
Db	181	qnikiqtlgtldklnlqgldkagldvdisgllsgtaaalvialadnaastakkvagafela	240							
Qy	181	QNIKGLGTLDKLNKGGLDKAGLDVLSGLSGATAALVIALADNAASTAKKVAGAFELA	240							
Db	241	nqvvgnitkavessyliaqrvaaaglstgtpvaalialstvsaisplafagladkfnhaks	300							
Qy	241	NQVVGNITKAVSSYILAQRVAAGLSSTGTPVAALIASTVSLAISPLAFAGTADKFNHAKSL	300							
Db	301	esyaerfkklygdgnlnlaeygrgtitdasvtaintaalaataggvsaaaagsviaspia	360							
Qy	301	ESYAEFRKKLYGDDNLLAEYGRGTITDASVTAINTAALAAIAGGVSAAAAGSVIASPIA	360							
Db	361	llysgitgvisitilyqskqamfehvankhnkiveknghknyfengydarylanlqd	420							
Qy	361	LLYSGITGVISTILYQSKAMFEHVANKHNKIVEKNHGNKNYFENGYDARYLANLQD	420							
Db	421	nmkfllnlkelqaerviaitqgqwdnnlgdlagisrlgekvlskayvdafeegkhika	480							
Qy	421	NMKFLLNLKELQAERVIAITQQWDNNIGDLAGISRLGEKVL SKAYVDAFEEGKHICA	480							
Db	481	dklvqldsangiidvnsngkaktqchlftpltpgtehrervqtgkyeyitklnlnrvd	540							
Qy	481	DKLVQDLSANGIIDVNSGKAKTQHILFTPLTPGTEHRERVQTGKYEYITKLNINRVD	540							
Db	541	swkitdgaasstdlcnvvqrigielidnagnvctketkilaiklgegdndnvfvgsgttei	600							
Qy	541	SWKITDGAASSTDLCNVVQRIEIDNAGNVCTKETKILAKLGEGDNDNVFVGSSTTEI	600							
Db	601	dgggydyrvhysrgnygalitadkatetedgysytnrvfetgkalhevtathalvgnree	660							
Qy	601	DGGEYDYRVHYSRGNYGALITADKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE	660							
Db	661	kieyrhsnqhaggytkdtlkaveeisigtshndifksgkndafnggdvdiidngdn	720							
Qy	661	KIEYRHSNQHAGGYTKDTLKAVEEISGTSHTNDIFPKSGKNDAFNGGDVDTIDNGDN	720							
Db	721	drifgqkgddildegngddfidgqkndllhgqkgddifvhrkgdndiidtsdgnkcls	780							
Qy	721	DRIFGKGDDILDEGNGDDFIDGKGNDLLHGKGDDIFVHRKGNDIIDTSDGNDKCLS	780							
Db	781	fsdsnlklditfekvkhnlvitnskkvktiqnwrfreadfakvypnykatkdekieleliq	840							
Qy	781	FSDSNLKDLITFEKVKNLVTNSKKVKTIQNWRFREADFAKEVPNYKATKDEXIEELIQ	840							
Db	841	ngerritskvddliakngkitdelskvvdnyellkhsknvtnsldklssvsafstsn	900							
Qy	841	NGERRITSKVDDLIKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFAFTSSN	900							
Db	901	dsrnvlvaptsmldqslsslqfargqhsyglrpg	936							
Qy	901	DSRNLVAPTSMLDQSLSSLQFARGQHSYGLRPG	936							

RESULT

2

ID

R34547 standard; Protein; 936 AA.

AC

R34547;

DT

23-AUG-1993 (first entry)

DE

GnRH-leukotoxin gene fusion prod.

KW

Vector; LKT 352; flanking; recombinant; antigen; somatostatin;

KW	gonadotropin releasing hormone; rotavirus viral protein 4 ;
KW	carrier protein; lactation; reproduction; SRIF.
OS	Synthetic.
FH	Key
FT	Location/Qualifiers
FT	protein 1..926
FT	peptide /note= "recombinant leukotoxin protein"
FT	927..936
FT	/note= "GnRH"
WO	9308290-A.
PN	29-APR-1993.
PD	13-OCT-1992.
PF	CA0449.
PR	16-OCT-1991; US-779171.
PR	14-OCT-1992; US-960932.
PR	(UYSA-) UNIV SASKATCHEWAN.
PI	Hughes HPA, Potter AA, Redmond MJ;
PI	WPI; 93-152482/18.
DR	N-PSDB; Q41322.
DR	Immunological carrier system with enhanced immunogenicity -
PT	comprises chimeric protein comprising leuco:toxin peptide or
PT	homologous protein fused to antigen esp. somatostatin or
PT	gonadotropin releasing hormone
PT	Example 2; Fig 8; 95pp; English.
PS	CC Oligonucleotides contg. sequences from bovine gonadotropin
CC	releasing hormone (GnRH) gene were constructed on a Pharmacia Gene
CC	assembler using standard phosphoramidite chemistry. The oligo-
CC	nucleotides were annealed and ligated into vector pAA352 (contg.
CC	the Pateurella haemolytica leuco-toxin gene) which had been digested
CC	with BamHI. The ligated DNA was used to transform E. coli strain
CC	MH3000. Transforms contg. The oligonucleotide inserts were
CC	identified by restriction endonuclease mapping and the recombinant
CC	plasmid designated pAA502. The chimeric protein produced from the
CC	plasmid works to bring about a larger immune response than the antigen
CC	alone, i.e. the leukotoxin works as a carrier protein.
CC	See also R34545-8.
CC	Sequence 936 AA.
SQ	

[illegible]

RESULT	2
ID	R34547
AC	R34547
DT	23-AUG
DE	GnRH-16
KW	vector

481 DKLVQDLSANGIIVDSNGRAKTHILFRPLTPTGEHERVQTKYEYITKLNINRVD 540
 541 switdgaastfdltntvgrigeldnagnvktketkiaklgdgdndvfgsgttei 600
 541 SWKIDGAASSTFDLTNVQRIEILDNAGNVTKTETKIIAKLGECDNDNVFGSGTTEI 600
 601 dgegdyrvhysgnygalcidakatetegsvtnrfvetgkalhevtsthtalvgnree 660
 601 DGEEDYRVHYSNGYVGNALCIDAKATETEGSVTNRFVETGKALHEVTSTHTALVGNREE 660
 661 kievhrsnqhagvytkdtikaveeligtshndifksgkfnafnggdvdtidngdn 720
 661 KIEYHRSNQHAGVYTKDTIKAVEELIGTSHNDIFKSGKFNDAFNGGDVDTIDNGDN 720
 721 drlfgkgddildggngddfidgkgkndllhggkgddifvhrkgdndliitdsdgnkls 780
 721 DRLFGKGDDILDGGNGDDFIDGKGKNDLLHGGKGDDIFVHRKGDDNDIITDSDGNKLS 780
 781 fdsnlikdlitfekvkhnlvitnskekvtignvfreafakevnpnykatdekiesiig 840
 781 FDSNLKDLITFEKVKHNLVITNSKEKVTIGNVFREADFKEVNPNYKATDEKIEIIG 840
 841 ngeritskvddliakngkitdeliskvndvnyellkshkntvnsldklissysaftsn 900
 841 NGERITSKVDDLIKNGKITDELISKVNDVNYELLKSHKNTVNSLDKLISSYSAFTSN 900
 901 dsrnvlvaptmsldqslslqfargshwsgylrpg 936
 901 DSRNLVAPTMSLDQSLSLQFARGSHWSGYGLRPG 936

RESULT 3

ID R52748 standard; Protein; 1069 AA.
 AC R52748;
 DT 01-JUL-1994 (first entry)
 DE Bovine IFNgamma/LKT chimeric protein encoded by plasmid pAA497.
 KW Bovine; interleukin-2; IL2; P. haemolytica; leukotoxin; LfK; IFN;
 KW ltkA; chromosome walking; fusion protein; vaccine; interferon; gamma;
 KW monoclonal; polyclonal; antibody.
 OS Pasteurella haemolytica - chimera
 OS Bos taurus - chimera.
 FH Key Location/Qualifiers
 FT peptide 1..926
 FT /note= "Recombinant leukotoxin peptide [split]"
 FT peptide 927..1069
 FT /note= "Bovine IFNgamma"
 FT US5273889-A.
 PN 28-DEC-1993.
 PD 22-AUG-1990; 571301.
 PF 22-AUG-1990; US-571301.
 PR 16-OCT-1991; US-777715.
 PA (CIBA) CIBA GEIGY CANADA LTD.
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Campos M, Hughes HPA, Potter A;
 DR WPI; 94-006587/01.
 DR N-PSDB; Q54213.
 PT Immunogenic fusion proteins of gamma-interferon and immunogenic
 PT leukotoxin - used in vaccines and to raise monoclonal and polyclonal
 PT antibodies
 PS Disclosures; Fig 7; 56pp; English.
 CC This sequence represents a fusion between bovine gamma interferon
 CC (IFNgamma) and Pasteurella haemolytica leukotoxin (LTK). The
 CC leukotoxin gene, ltkA, was isolated from a gene library of P.
 CC haemolytica by chromosome walking. Immunogenic fusion proteins
 CC such as this can be used in vaccine compositions. It can also be
 CC used to raise mono- and polyclonal antibodies.
 SQ Sequence 1069 AA;

Query Match 98.7%; Score 6135; DB 9; Length 1069;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidlsfpktgakkiliipnqvdyteqngldlvkaaeelgievqreennia 60
 QY 1 MATVIDLSFPKTKAKKILIIIPONTQYDTEQNGLDLVKAAEELGIEVQREENNIA 60
 Db 61 qtslgtiqtaigtergivlsapqdkllqtkagaglaesivgnanaktvlsigsgs 120
 QY 61 QTSLGTIQTAIGTERGIVLSAPQDKLLQTKAGAGLAESI VGNANKAKTVLSIGSGS 120
 Db 121 llsvglamdldealnnsnqhalakagletltnslieniansvktldefgeqisqfsgkl 180
 QY 121 ILSVGLAMDLDEALNNSNQHALAKAGLETLSNTIENTIANSVKTLDEFGEQISQFSGKL 180
 Db 181 qniklgtlqdklknigldkagldvlsqllsqataalvldknastakvqagfela 240
 QY 181 QNIKLGTLQDKLKNIGLDKAGLDVLSQLLSQATAALVLDKNASTAKVQAGFELA 240
 Db 241 ngvvgnitkavasyilaqrvaaaglstgtpvaalastvslafagladkfnhaki 300
 QY 241 NGVVGNTITKAVSSYILAQRVAAAGLSTGTPVAALASTVSLAISPFAFAGIADKFNHAKSL 300
 Db 301 esyaerfkklgydgnlllaeygrtgtidasvtaintalaaaggvsaaagsvlaspia 360
 QY 301 ESYAERFKKLGYDGNLLAEYQRTGTIDASVTAINTALAAAGGVSAAGSVIASPIA 360
 Db 361 llvsgitgvisitlqyskcamfehvankihkiveeknnhknfyfengydarylanld 420
 QY 361 LLVSGITGVISTILQYSKCAMFEHVANKIHKIVEEKNHKNFYFENGYDARYLANLD 420
 Db 421 nmkflnltnkelaerviaitqgqvdnllqdlagisrlgekvlsqkayvdafeegkhika 480
 QY 421 NMKFLNLTNKELQAEVIAITQQQDNNIGDLAGISRLGEKVLSQKAYVDAFEEGKHIIKA 480
 Db 481 dkvlqdsanglidvsnsgaktqhilfrtlltpgtehrervvtgkyeyitklninrvd 540
 QY 481 DKLVQLDSANGIIDVSNSGAKTQHILFRTPLLTPGTEHRERVQTKYEYITKLNINRVD 540
 Db 541 swkitdgaastfdltntvgrigeldnagnvktketkiaklgdgdndvfgsgttei 600
 QY 541 SWKIDGAASSTFDLTNVQRIEILDNAGNVTKTETKIIAKLGECDNDNVFGSGTTEI 600
 Db 601 dgegdyrvhysgnygalcidakatetegsvtnrfvetgkalhevtsthtalvgnree 660
 QY 601 DGEEDYRVHYSNGYVGNALCIDAKATETEGSVTNRFVETGKALHEVTSTHTALVGNREE 660
 Db 661 kievhrsnqhagvytkdtikaveeligtshndifksgkfnafnggdvdtidngdn 720
 QY 661 KIEYHRSNQHAGVYTKDTIKAVEELIGTSHNDIFKSGKFNDAFNGGDVDTIDNGDN 720
 Db 721 drlfgkgddildggngddfidgkgkndllhggkgddifvhrkgdndliitdsdgnkls 780
 QY 721 DRLFGKGDDILDGGNGDDFIDGKGKNDLLHGGKGDDIFVHRKGDDNDIITDSDGNKLS 780
 Db 781 fdsnlikdlitfekvkhnlvitnskekvtignvfreafakevnpnykatdekiesiig 840
 QY 781 FDSNLKDLITFEKVKHNLVITNSKEKVTIGNVFREADFKEVNPNYKATDEKIEIIG 840
 Db 841 ngeritskvddliakngkitdeliskvndvnyellkshkntvnsldklissysaftsn 900
 QY 841 NGERITSKVDDLIKNGKITDELISKVNDVNYELLKSHKNTVNSLDKLISSYSAFTSN 900
 Db 901 dsrnvlvaptmsldqslslqfargsg 927
 QY 901 DSRNLVAPTMSLDQSLSLQFARGSG 927

RESULT 4

ID W13867 standard; Protein; 1069 AA.
 AC W13867;
 DT 12-MAY-1997 (first entry)
 DE Chimeric protein #2.
 KW RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
 KW interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
 KW Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;

KW fibrinous pneumonia; cattle; therapy.

OS Synthetic.
 PN US5594107-A.
 PD 14-JAN-1997.
 PR 22-AUG-1990; 571301.
 PR 22-AUG-1990; US-571301.
 PR 16-OCT-1991; US-777715.
 PR 20-DEC-1993; US-170126.
 PA (CIBA) CIBA GEIGY CANADA LTD.
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Campos M, Hughes HPA, Potter A;
 DR WPI: 97-099529/09.
 DR N-PSDB: T60033.
 PT Immunogenic chimeric proteins comprising cytokine linked to RTX
 toxin - useful in vaccines, esp. against shipping fever in cattle
 PS Claim 13; Column 37-46; 56pp; English.
 CC W13866 and W13867 represent immunogenic chimeric proteins of the
 CC invention. This sequence represents a chimeric protein containing the
 CC bovine gamma interferon (gamma IFN) sequence and a leukotoxin sequence.
 CC The chimeric proteins of the invention comprise a cytokine, selected from
 CC interleukin-2 (IL-2) and gamma IFN, linked to at least one RTX toxin
 CC epitope (preferably the sequence shown in W13865). The RTX toxin used to
 CC provide the epitope sequence is preferably a leukotoxin, especially the
 CC full-length Pasteurella haemolytica leukotoxin. Alternatively, the
 CC leukotoxin is a truncated leukotoxin lacking leukotoxic activity,
 CC especially LKT352. The chimeric proteins can be used for the production
 CC of vaccines against respiratory diseases such as pneumonia, particularly
 CC fibrinous pneumonia caused by P.haemolytica, including shipping fever in
 CC cattle.
 SQ Sequence 1069 AA;

Query Match 98.7%; Score 6135; DB 21; Length 1069;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidlsfpktgakkililypqnyqydtgnglqdlvkaaeelgievqreernniata 60
 |||||||
 QY 1 MATVIDLSFPKTGAKKILILYPQNYQYDTGNGLQDLVKAEEELGIEVQREERNIATA 60
 |||||||
 Db 61 qtslgtqtaigttergvlspaptdklqlktkagaglaesivqnankaktvlsqigs 120
 |||||||
 QY 61 QTSLGTQTAIGTTERGIVLSAPQIDKLQKTQKAGALSAESIVQNANKAKTVLSGIQS 120
 |||||||
 Db 121 ilqsvlagmdlealqnnsqhalakagteltnslieniansvktldfegdisfgskl 180
 |||||||
 QY 121 ILQSVLAGMDLEALQNNSENQHALAKAGTELNSLIENIANSVKTLDFEGDISFGSKL 180
 |||||||
 Db 181 qnikgltgldklnigglidkaglgldvisgllsgataalvialadknastakkvagafela 240
 |||||||
 QY 181 QNIKGLTGLDKLKNIGGLDKAGLGLDVISGLLSGATAALVIALADKNASTAKKVAGAFELA 240
 |||||||
 Db 241 nqvgnitkavssyllaqraaglstgtpvaalilstvslaisplafagiadkfahksl 300
 |||||||
 QY 241 NQVGNITKAVSSYILAQRAAGLSTGTPVAALIASTVSLAISPLAFAGIADKFHAKSL 300
 |||||||
 Db 301 esvaerfkklygdgnllaeaygrgtidasytaintalaaialaggvsaaasvlaspia 360
 |||||||
 QY 301 ESAERFKKLYGDGNLLAEYGRGTIDASYTAINTALAAIAGGVSAAASVTASPIA 360
 |||||||
 Db 361 livsgitgvtistilqyskamfehvanikhkivveknhghknfyfengydarylanlqd 420
 |||||||
 QY 361 LLVSGITGVISTILQYSKAMFEHVANKIHKIVVEKNHGHKNFYFENGYDARYLANLQD 420
 |||||||
 Db 421 nmkflnlmkelaerviaitgqqvddnngldlaglsrlgkvlsgkayvdafeegkhika 480
 |||||||
 QY 421 NMKFLNLNKLQAEVIAITQQVDDNNGLDLAGLSRLGKVLSGKAYVDAFEEGKHika 480
 |||||||
 Db 481 dklvqlidsangiidsnksaktqhlftpltpgttehrervqtkgyeyiklinirvd 540
 |||||||
 QY 481 DKLVLQDSANGIIDVNSKAKTQHLFTPLTPGTTEHREVRVQTKGYEYIKLINIRVD 540
 |||||||
 Db 541 swkitdgaasstfdltnvvqrglgieidnagnvktktetkiaaklgegdndnfvsggttei 600
 |||||||

QY 541 SWKITDGAASSTFDLTNNVQRIGIELDNAGNVTKTKETIIAKLGEEDDNVFGSGTTEI 600
 Db 601 dggegydrvrhysrgnygaltidatketegsytvnrnfvetgkalhevtsthtalvgnree 660
 |||||||
 QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTVNRFVETGKALHEVTSTHTALVGNREE 660
 |||||||
 Db 661 kievrhshnqhagyytkdtlkaveeiiigtshndifkgskfndafnggdvtdidngdn 720
 |||||||
 QY 661 KIEVRHSHNQHHAGYYTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGDVDTIDNGDN 720
 |||||||
 Db 721 drlfggkaddildgnggdfidgkgndllhggkgddifvhrkgdndiildsgndkls 780
 |||||||
 QY 721 DRLFGGKDDIILDGNGDDFIDGKGNDLLHGGKDDIFVHRKGDDIITDSGNDKLS 780
 |||||||
 Db 781 fsdnlkltfkvkhnlvitnskekvtlgnwfreadfakvnpnykatkdeleelgq 840
 |||||||
 QY 781 FSDNLKLTPEKVKHNLVITNSKEKVTIQNWFREADFAKEVNPYKATKDEIEEIIQG 840
 |||||||
 Db 841 ngeritsqvdllakngkitqdelkskvdyndyellhsknvtnsldklsvsafssn 900
 |||||||
 QY 841 NGERITSQVDDLLAKNGKITQDELSKVVDNYELLHSKNVTNSLDKLSVSAFTSSN 900
 |||||||
 Db 901 dsrnvlvaptsmldgslslgfgarsq 927
 |||||||
 QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927
 |||||||

RESULT 5

ID R14482 standard; Protein; 926 AA.
 AC R14482;
 DT 15-JAN-1992 (first entry)
 DE LKT352.
 KW Antigen; leukotoxin; vaccine; lktA.
 OS Pasteurella haemolytica.
 PN WO9115237-A.
 PD 17-OCT-1991.
 PE 17-OCT-1991; CA0170.
 PR 05-APR-1990; US-504850.
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Acres SD, Bariuk LA, Potter AA, Lawman MJP;
 DR WPI: 91-324967/44.
 PT Vaccines for Pasteurella haemolytica infection in cattle -
 PT comprise sub-unit antigens from P haemolytica fibrillar protein,
 PT plasmin receptor, 50 K outer membrane protein and leukotoxin.
 PS Disclosure; Fig 5; 92pp; English.
 CC LKT352 is 98% homologous with authentic leukotoxin and migrates
 CC to the same position on gels.
 CC The LKT352 gene was prep'd. as follows: lktA, an MaeI fragment
 CC contg. the gene was ligated into the SmaI site of pUC13 to form
 CC pAAL79. From this, two constructs were made in the pTac-based
 CC vector, pOH432:laci digested with SmaI. One, pAA342, consisted of
 CC the 5' AluII fragment from lktA while the other, pAA345, contained
 CC the entire MaeI fragment. Clone pAA342 expressed a truncated
 CC leukotoxin peptide at high levels while pAA345 expressed full
 CC length leukotoxin at very low levels. The 3' end of the lktA gene
 CC of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to
 CC yield pAA352 contg. the LKT352 sequence. The protein expressed
 CC from the vector can be used to prepare a subunit vaccine with
 CC other P. haemolytica antigens, e.g. fibrillar protein, plasmin
 CC receptor or 50K outer membrane protein. The vaccines can be used
 CC to protect cattle from respiratory diseases such as pneumonia, esp.
 CC shipping fever pneumonia.
 CC See also R14481, 83, 84 and 85.
 SQ Sequence 926 AA;

Query Match 98.6%; Score 6128; DB 3; Length 926;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidlsfpktgakkililypqnyqydtgnglqdlvkaaeelgievqreernniata 60
 |||||||
 QY 1 MATVIDLSFPKTGAKKILILYPQNYQYDTGNGLQDLVKAEEELGIEVQREERNIATA 60
 |||||||

```

Db 61 qtslgtiqtaiqtergvisapqldkllqktkagqalsaesivnankaktvlsqigs 120
QY 61 QTSLGTIQTAIQTERGIVISAPQIDKLLQKTKAGALGSAESIVNANKAKTVLSGIQS 120
Db 121 ilgsvlagmdldealqnnshqhalakagieltnslslieniansvktldefgeqisqfsgkl 180
QY 121 ILGSLVLAGMDLDEALQNNSHQHALAKAGIELTNSLIENIANSVKTLDGEQISQFSGKL 180
Db 181 qnikgltlqdklknlgldkaglgldvsgllsgataalvldacknastakvvgagfela 240
QY 181 QNIKGLTLDKLNKLGDLKAGLGLDVLSGLSGATAALVLDAKNASTAKVVGAGFEA 240
Db 241 nqvvgntkavssyilaqrvaaglstgtpvaalialastvslaisplafagladfnhaks 300
QY 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIAASTVSLAISPLAFAGLADFNHAKSL 300
Db 301 esyaerfklkgldgdnllaeyqrgrgtidastvtaintalaaaggvsaaagsviaspia 360
QY 301 ESYAERFKLKGVDGDNLLAEYQRGTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
Db 361 llvsgitgvtistilqyskqamfahvankhmkiveknnhngknyfengydarylanlqd 420
QY 361 LLVSGITGVTISTILQYSKQAMFEHVANKHMKIVEKNNHNGKNYFENGYDARYLANLQD 420
Db 421 nmkfllnlknelqaerviaitqqwddnngldagierlgekvlsqkayvdafegkhika 480
QY 421 NMKFLNLNKLQAEVIAITQQWDDNNGLDAGIERLGEKVLSQKAYVDAFEKGHIKA 480
Db 481 dklvqdsangliidvsnsgkaktqhlfrptlltpgtehrvrtgkyeytklnlnrvd 540
QY 481 DKLVLDSANGLIIDVSNSGKAKTQHLFRPTLLTPGTEHREVRTGKYEYTKLNINRVD 540
Db 541 switdgaastfdltnvgrigeldnagnvktketkilaiklgedgdndvfgsgttei 600
QY 541 SWITDGAASFTDLTNVGRIGELDNAGNVKTKETKIILAKLGEDGDNDVFGSGTTEI 600
Db 601 dgegdyrvhysrgnvgalidkatetegsvtnrvfetgkalhevtsthtalvgnree 660
QY 601 DGEGDYRVHYSRGNGVGAALIDKATETEGSVTNRVFETGKALHEVTSTHTALVGNREE 660
Db 661 kieyrhnnghagyyckdtlkaveeligtshndifksgkfnafnggdvtdidngdn 720
QY 661 KIEYRHSNNHAGYYCKDTLKAVEELIGTSHNDIFKSGKFNDFNGGDVTDIDNGDN 720
Db 721 drlfgkgddildgngddfdidgkgndllhggkgddifvhrkgdndliitdsdgnkls 780
QY 721 DRLFGKGDDILDGNGDDFDIDGKGNDLLHGGKGDDIFVHRKGDDNDIITDSGDNKLS 780
Db 781 fsdsnlkdltfekvkhnlvitnskekvtiqnwfreadfakvpykatkdeieeiigq 840
QY 781 FSDSNLKDITFEKVKHNLVITNSKEKVTIQNWFREADFAPKVPYKATKDEIEEIIQG 840
Db 841 ngeritskvddliakngkitdelkskvndyellkhsknvtnsidklissvsaftssn 900
QY 841 NGERITSKVDDLIKNGKITDELKSKVNDYELLKHSKNVTNSIDKLISSVSAFTSSN 900
Db 901 dsrnlvaptmsldqslsslfargs 926
QY 901 DSRNLVAPTMSLDQSLSSLFARGS 926

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RESULT 6

ID R34545 standard; Protein: 926 AA.

AC R34545;

DE Leukotoxin 352 produced from pAA352

KW Vector; LKT 352; flanking; recombinant; antigen; somatostatin;

KW gonadotropin releasing hormone; rotavirus viral protein 4;

KW carrier protein; lactation; reproduction.

OS Pasteurella haemolytica.

PN WO9308290-A.

PD 25-APR-1993.

PF 15-OCT-1992; CA0449.

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PR 16-OCT-1991; US-779171.
PR 14-OCT-1992; US-960932.
PA (UYSA-) UNIV SASRATCHEWAN.
PI Hughes HPA, Potter AA, Redmond MJ;
DR WPI; 93-152482/18.
DR N-PSDB; Q41317.
PT Immunological carrier system with enhanced immunogenicity -
PT comprises chimeric protein comprising leuco:toxin peptide or
PT homologous protein fused to antigen esp. somatostatin or
PT gonadotropin releasing hormone
PS Disclosure; Fig 3; 95pp; English.
CC Gene libraries of P. haemolytica A1 (strain B122) were constructed
CC in lambda gt11 and pUC13. Resulting clones were used to transform E.
CC coli and individual colonies were pooled and screened for reaction
CC with serum from a calf which had survived a P. haemolytica infection
CC and that had been boosted with a conc. culture supernatant of P.
CC haemolytica to increase anti-leukotoxin antibody levels. Positive
CC colonies were screened for their ability to produce leukotoxin by
CC incubating cell lysates with bovine neutrophils and measuring the
CC release of lactate dehydrogenase from the neutrophils. A 4kb
CC fragment was obtd. Progressively larger clones were isolated by
CC chromosome walking to isolate full length recombinants of ca. 8kb,
CC in pAA114. The clone was subjected to restriction enzyme digestion
CC to yield two clones, one expressing truncated leukotoxin peptide at
CC high levels and the other expressing the full length leukotoxin at
CC low levels. The 3' end of the lktA gene from the full length clone
CC was ligated to the truncated gene clone to yield plasmid pAA352. The
CC clone was used to produce chimeric proteins by gene fusion with an
CC antigen coding sequence, e.g. the coding sequence of somatostatin,
CC gonadotropin releasing hormone or rotavirus viral protein 4, i.e.
CC leukotoxin works as a carrier protein to bring about a larger
CC immune response than the antigen alone. Immunisation with these
CC antigens can regulate growth rate, lactation and reproductive efficiency.
CC See also R34546-8.
SQ Sequence 926 AA;

```

Query Match 98.6%; Score 6128; DB 7; Length 926;

Best Local Similarity 100.0%; Pred. NO. 0.00e+00;

Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 1 matvidlsfpktgakkililvipqnydteqngldlvkaaeelgievqreenniata 60
QY 1 MATVIDLSFPKTGAKKILILVIPQNYDTEQNGLDLVKAAEELGIEVQREENNIATA 60
Db 61 qtslgtiqtaiqtergvisapqldkllqktkagqalsaesivnankaktvlsqigs 120
QY 61 QTSLGTIQTAIQTERGIVISAPQIDKLLQKTKAGALGSAESIVNANKAKTVLSGIQS 120
Db 121 ilgsvlagmdldealqnnshqhalakagieltnslslieniansvktldefgeqisqfsgkl 180
QY 121 ILGSLVLAGMDLDEALQNNSHQHALAKAGIELTNSLIENIANSVKTLDGEQISQFSGKL 180
Db 181 qnikgltlqdklknlgldkaglgldvsgllsgataalvldacknastakvvgagfela 240
QY 181 QNIKGLTLDKLNKLGDLKAGLGLDVLSGLSGATAALVLDAKNASTAKVVGAGFEA 240
Db 241 nqvvgntkavssyilaqrvaaglstgtpvaalialastvslaisplafagladfnhaks 300
QY 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIAASTVSLAISPLAFAGLADFNHAKSL 300
Db 301 esyaerfklkgldgdnllaeyqrgrgtidastvtaintalaaaggvsaaagsviaspia 360
QY 301 ESYAERFKLKGVDGDNLLAEYQRGTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
Db 361 llvsgitgvtistilqyskqamfahvankhmkiveknnhngknyfengydarylanlqd 420
QY 361 LLVSGITGVTISTILQYSKQAMFEHVANKHMKIVEKNNHNGKNYFENGYDARYLANLQD 420
Db 421 nmkfllnlknelqaerviaitqqwddnngldagierlgekvlsqkayvdafegkhika 480
QY 421 NMKFLNLNKLQAEVIAITQQWDDNNGLDAGIERLGEKVLSQKAYVDAFEKGHIKA 480
Db 481 dklvqdsangliidvsnsgkaktqhlfrptlltpgtehrvrtgkyeytklnlnrvd 540

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QY 481 DKLVQDSANGIIVDSNSKAKTQHILFPLLTGTEHRRVQKVEYITKLNINRVD 540.
|||||
Db 541 swkitdgaasftdlnvvqrvgldnagnvktktetkilaaklgdgdndvfvsggttei 600
|||||
QY 541 SNKITDGAASFTDLTNVVQRIGIELDNAGNVTKTETKIIAKLGEQDNDVFGSGTTEI 600
|||||
Db 601 dggegydrvhysrgnygaltidatketegsytvnrftvetgkalhevsthtalvgnree 660
|||||
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTVNRFVETGKALHEVSTHTALVGNREE 660
|||||
Db 661 kleyrhshnnqhagvytkdtikaveeiiqtsghndifksgkfndafngdgvdtidgndgn 720
|||||
QY 661 KLEYRHSNNQHAGVYTKDTLKAVEEIIQTSGHNDIFKSGKFNDAFNGDGVDTIDGNDGN 720
|||||
Db 721 drlfggkgddiildgngddfidggkgndllhggkgddifvhrkgdndiildtsdgnkls 780
|||||
QY 721 DRLFGGKGDDIILDGNGDDFIDGGKGNLLHGGKGDDIFVHRKGDNDIILDSDGNKLS 780
|||||
Db 781 fdsnlkdltfekvkhnlvntsktektvtiqnwfreafakevpykatkdekieleiigq 840
|||||
QY 781 FSDSNLKDLTFEKVKHNLVNTSKTEKVTIQNWFREADFKEVPYKATKDEKIEEIIIGQ 840
|||||
Db 841 ngeritskvddliakngkitqgdelskvvdnyellkshknvntslkklissvsafstsn 900
|||||
QY 841 NGERITSKVDDLIKANGKITQDELSKVVDNYELLKSHKNVTNSLDKLISSVSFTSSN 900
|||||
Db 901 dsrnvlvaptsmldqslsllqfargs 926
|||||
QY 901 DSRNVLVAPTSMLDQSLSLQFARGS 926
|||||

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RESULT 7

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ID R50291 standard; Protein: 926 AA.
AC R50291;
DE 06-OCT-1994 (first entry)
DE Recombinant leukotoxin from plasmid PAA352.
KW Vaccine; outer membrane protein; OMP; Haemophilus somnus;
KW iron regulated protein; leukotoxin; Pasteurella haemolytica;
KW LKt352.
KW Pasteurella haemolytica A1 (strain B122).
PS CA2099707-A.
PD 03-JAN-1994.
PE 29-JUN-1993; 099707.
PR 02-JUL-1992; US-908253.
PA (UYSA-) UNIV SASKATCHEWAN.
PI Harland RJ, Potter AA;
DR WPI: 94-092909/12.
DR N-PSDB: Q44760.
PT Haemophilus somnus outer membrane protein extract -
PT enriched with iron-regulated proteins, opt. contg.
PT leuco:toxin antigens, for use as vaccine
PS Claim 5; Fig 5; 78pp; English.
CC A vaccine comprising an outer membrane protein (OMP) extract of
CC Haemophilus somnus enriched with iron regulated proteins is new.
CC The vaccine pref. further comprises an immunogenic leukotoxin
CC polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin
CC homologous to LKt352. Example 1.2 describes the prodn. of
CC P. haemolytica recombinant leukotoxin from PAA352.
CC Two expression constructs were made. One, PAA342, contained the
CC 5'-AhaiI fragment of the lktA gene, while the other, PAA345,
CC contained the entire lktA gene. PAA342 expressed a truncated
CC leukotoxin peptide at high levels, while PAA345 expressed full
CC length leukotoxin at very low levels. Therefore, the 3' end
CC of the lktA gene was ligated into PAA342, yielding plasmid PAA352.
CC LKt352 or new leukotoxin is 98% homologous to authentic
CC leukotoxin.
CC NB: the protein sequence in Fig 5 comprises 926 amino acids,
CC however this protein is described in the text as having
CC 931 amino acids.
SQ Sequence 926 AA;

```

Query Match 98.6%; Score 6128; DB 10; Length 926;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 1 matvidlsfptgakkliilypqnyqydtengnglqdlvkaaeelgievqreernniata 60
|||||
QY 1 MATVIDLSFPTGAKKLIILYPQNYQYDTEGNGLQDLVKA AEELGIEVQREERNNIATA 60
|||||
Db 61 qtslgtlqtaigltergivilsapqldkllqtkkagqalgsaeslvqnankaktvlsqigs 120
|||||
QY 61 QTSLGTQTQTALGLTERGIVLSAPQIDKLLQTKRAGQALGS AESIVQNANKAKTVLSGTQS 120
|||||
Db 121 ilgsvlaqmdldealaqnnsqhalakagleltnslieniansvktldfegqisqfsgskl 180
|||||
QY 121 ILGSVLAGMDLDEALQNNNOHALAKAGLELTNSLIENIAN SVKTLDFEGQISQFSGSKL 180
|||||
Db 181 qnikglgtlqdklnigldkagldgldvisgllsqataalvlnadknastakkvagfela 240
|||||
QY 181 QNIKGLGTLDKLNIGGLDKAGLDLVISGLLSGATAALV LADKNASTAKKVAGFELA 240
|||||
Db 241 nvvgvntkavssyilaqrvaaglsstgppvaallastvslaisplafagladkfnhaksl 300
|||||
QY 241 NOVVGVNITKAVSSYILAQ RVAAGLSSTGPPVAALAST VSLAISPLAFAGIADKFENHAKSL 300
|||||
Db 301 esyvaerfkkgldgdnllaevgrgtgtidasvtaintalaaiaagvsaagviapla 360
|||||
QY 301 ESYVAERFKLGDGDNLLAEVGRGTGTIDASVTAIN TALAAIAGVSAAGVIAPIA 360
|||||
Db 361 llvgitgvisitliqyskqamfehvankhknkiveweknnhknkfengydarylanlqd 420
|||||
QY 361 LLVGSITGVISTILQYSKQAMFEHVANKHNKIV EWEKNNHKNKFENGYDARYLANLQD 420
|||||
Db 421 nmkfllnlnkelqaerviaitcqqgdnnnigdlaglsrlgekvlsqkayvdafeegkhika 480
|||||
QY 421 NMKFLLNLNKE LQAERVIAITCQQGDNNNIGDLA GLSRLGEKVLSQKAYVDAFEEGKHIKA 480
|||||
Db 481 dklvqlsdanglidvsnsgkaktchilfrtlltpgtrehervotgkveytktninrvd 540
|||||
QY 481 DKLVQLSDANGLIDVSNSGKAKTQHILFRTPLLTPGT REHREVOTGKVEYITKLNINRVD 540
|||||
Db 541 swkitdgaasftdlnvvqrvgldnagnvktktetkilaaklgdgdndvfvsggttei 600
|||||
QY 541 SWKITDGAASFTDLTNVVQRIGIELDNAGNVTKTET KIIAKLGEQDNDVFGSGTTEI 600
|||||
Db 601 dggegydrvhysrgnygaltidatketegsytvnrftvetgkalhevsthtalvgnree 660
|||||
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEGSYTVNRF VETGKALHEVSTHTALVGNREE 660
|||||
Db 661 kleyrhshnnqhagvytkdtikaveeiiqtsghndifksgkfndafngdgvdtidgndgn 720
|||||
QY 661 KLEYRHSNNQHAGVYTKDTLKAVEEIIQTSGHND IFKSGKFNDAFNGDGVDTIDGNDGN 720
|||||
Db 721 drlfggkgddiildgngddfidggkgndllhggkgddifvhrkgdndiildtsdgnkls 780
|||||
QY 721 DRLFGGKGDDIILDGNGDDFIDGGKGNLLHGGKGDD IFVHRKGDNDIILDSDGNKLS 780
|||||
Db 781 fdsnlkdltfekvkhnlvntsktektvtiqnwfreafakevpykatkdekieleiigq 840
|||||
QY 781 FSDSNLKDLTFEKVKHNLVNTSKTEKVTIQNW FREADFKEVPYKATKDEKIEEIIIGQ 840
|||||
Db 841 ngeritskvddliakngkitqgdelskvvdnyellkshknvntslkklissvsafstsn 900
|||||
QY 841 NGERITSKVDDLIKANGKITQDELSKVVDNYELL KSHKNVTNSLDKLISSVSFTSSN 900
|||||
Db 901 dsrnvlvaptsmldqslsllqfargs 926
|||||
QY 901 DSRNVLVAPTSMLDQSLSLQFARGS 926
|||||

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RESULT 8
ID R42378 standard; Protein: 924 AA.
AC R42378;
DT 19-APR-1994 (first entry)
DE Recombinant leukotoxin peptide (split) from plasmid pGCH5.

KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
 KW thromboembolic meningococcal septicemia; arthritis;
 KW pneumonia; lktA gene; haemin-binding protein; fusion protein.
 OS Pasteurella haemolytica.
 PN W09321323-A.
 PD 28-OCT-1993.
 PF 05-APR-1993; CA0135.
 PR 09-APR-1993; US-865050.
 PR 04-JUN-1992; US-893424.
 PR 04-JUN-1992; US-893426.
 PR 29-MAR-1993; US-038287.
 PR 29-MAR-1993; US-038288.
 PR 29-MAR-1993; US-038719.
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 DR N-PSDB; Q51081.
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA
 PS Disclosure; Fig 5; 119pp; English.
 CC The hmb gene encoding the haemin-binding protein was expressed in
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
 CC lktA coded for by plasmid pAA352. The hmb gene fragment was taken
 CC from PRAP501 and starts at the codon for the third amino acid residue
 CC of ORF1. The haemin binding protein can be used in vaccines for
 CC preventing or treating H. somnus infections, which cause thromboembolic
 CC meningococcal septicemia, arthritis and pneumonia in
 CC vertebrates.
 CC See also R42370-86.
 SQ Sequence 924 AA;
 Query Match 98.4%; Score 6117; DB 8; Length 924;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 matvidsfpktaakliipqnyqdyteqngldlvkaaeelgievqreennia 60
 QY 1 MATVIDLSFPKTAAGKLIIPQNYQDYTEQNGLDLVKAAEELGIEVQREENNIA 60
 Db 61 qtslgtiqtaigtergivilsapqdklqktkagalgasvgnpankaktvslgigs 120
 QY 61 QTSLGTIQTAIGTERGIVLSAPQDKLQKTKAGALGASVGNPANAKKTVSLGIGS 120
 Db 121 ilgsvlagmdldealqnshqhalakagleitnslieniansvktldefgeqisqfsgkl 180
 QY 121 ILGSLAGMDLDEALQNSNOHALAKAGLEITNSLIENIANSVKTLDEFGEQISQFSGKL 180
 Db 181 qnikgltgdklknigldkagldgldvsgllsgataalvldadknaastakkvagfela 240
 QY 181 QNIKGLTGDKLKNIGLDKAGLDGLDVSGLLSGATAALVLDADKNASTAKKVAGFELA 240
 Db 241 nqvvgntkavssvllaqrvaaglstgqpvaaliastvslaisplafagiadkfnhaks 300
 QY 241 NOVVGNTKAVSSVLLAQRVAAGLSSTGQPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
 Db 301 esyaerfkllgydgnllaeyqrgrgtgtidasvtaintalaaiggyvsaaagsviaspia 360
 QY 301 ESYAERFKLLGYDGNLLAEYQRGRGTGTIDASVTAIN TALAAIGGYVSAAAGSVIASPIA 360
 Db 361 llvsgitgvtistilqyskqamfahvankhmkiveknhngknyfengydarylanlqd 420
 QY 361 LLVSGITGVTISTILQYSKQAMFAHVANKHMKIVEKNHNGKNYFENGYDARYLANLQD 420
 Db 421 nmkflnlnkelcaervialtqgqndnldlagisrlgekvlskayvdafegkthika 480
 QY 421 NMKFLNLNKELCAERVIALTQGGQNDNLDLAGISRLGEKVLSKAYVDAFEGKTHIKA 480
 Db 481 dklvqidsangiidvsnsgkaktqhlfrptlltpgttehrvrtgkyeyitklninrvd 540
 QY 481 DKLVLQDSANGIIDVSNSGKAKTQHILFRPTLLTPGTEHREVRTGKYEYITKLNINRVD 540

Db 541 swkitdgaasstfdltnvqvrigieldnagnvktkktkialkagddnfvsgattei 600
 QY 541 SWKITDGAASSTFDLTNVQVRIGIELDNAGNVTKTETIIAKLGGDDNVFVSGTTEI 600
 Db 601 dggegydrvhyrgnygaltidatketegsytvnrftvetgkalhevtsthalvgnree 660
 QY 601 DGGEGYDRVHYSRGNYGALTIDATKETECSYTVNRFVETGKALHEVSTHTALVGNREE 660
 Db 661 kleyrhnsnqhagyytktklkaeveiigtshndlfksgkfndafnggvgvtdidngdn 720
 QY 661 KIEYRHSNNQHAGYYTKTKLKAVEEIIIGTSHNDIFKSGKFNDAFNGGVGVDIDNGDN 720
 Db 721 drlfsgkgddilidgngddfidgkgndilhqgkddifvhrkgdndiitdsdngdkls 780
 QY 721 DRLFGKGDDIILIDGNGDDFIDGKGNDILHQGKDDIFVHRKGNDIITDSDGNDKLS 780
 Db 781 fdsnlkdlitfekvkhnlvitnskkvktiqnwfreadfakvnpnykatkdekiesliqg 840
 QY 781 FSDSNLKDLITFEKVKNLVTNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 Db 841 ngeritskvddliakngkitqdelskvyvnyellkhsknvtnsldklissvsaftsn 900
 QY 841 NGERITSKVDDLIKNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISVSFAFTSN 900
 Db 901 dsrnvlvaptmsldqslslqfar 924
 QY 901 DSRNVLVAPTMSLDQSLSLQFAR 924
 RESULT 9
 ID R42380 standard; Protein; 924 AA.
 AC R42380;
 DT 19-APR-1994 (first entry)
 DE Recombinant leukotoxin peptide (split) from plasmid pGCH4.
 KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
 KW thromboembolic meningococcal septicemia; arthritis;
 KW pneumonia; lktA gene; haemin-binding protein; fusion protein.
 OS Pasteurella haemolytica.
 PN W09321323-A.
 PD 28-OCT-1993.
 PF 05-APR-1993; CA0135.
 PR 09-APR-1993; US-865050.
 PR 04-JUN-1992; US-893424.
 PR 04-JUN-1992; US-893426.
 PR 29-MAR-1993; US-038287.
 PR 29-MAR-1993; US-038288.
 PR 29-MAR-1993; US-038719.
 PA (UYSA-) UNIV SASKATCHEWAN.
 PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
 PI Rioux C, Theisen M;
 DR N-PSDB; Q51082.
 PT Haemophilus somnus immunogenic proteins used in vaccines -
 PT selected from haemin-binding protein, haemolysin, LppB and LppC,
 PT and corresp. DNA
 PS Disclosure; Fig 6; 119pp; English.
 CC The hmb gene encoding the haemin-binding protein was expressed in
 CC E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene
 CC lktA coded for by plasmid pAA352. The hmb gene fragment was taken
 CC from PRAP504 and starts at the codon for the 33 rd amino acid residue
 CC of ORF1. The haemin binding protein can be used in vaccines for
 CC preventing or treating H. somnus infections, which cause thromboembolic
 CC meningococcal septicemia, arthritis and pneumonia in
 CC vertebrates.
 CC See also R42370-86.
 SQ Sequence 924 AA;
 Query Match 98.4%; Score 6117; DB 8; Length 924;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 matvidsfpktaakliipqnyqdyteqngldlvkaaeelgievqreennia 60
 QY 1 MATVIDLSFPKTAAGKLIIPQNYQDYTEQNGLDLVKAAEELGIEVQREENNIA 60

```
QY 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEQNGQLDLVKAABEELGIEVQREERNNIATA 60
Db 61 qtslgtigtaltgtergvlslapqldkllqktkagaglaesaesivqnankaktvlsqigs 120
QY 61 QTSLGITQTAIGLTERGIVLSAPQIDKLLQKTKAGQALGSAESIVQNANKAKTVLSGIQS 120
Db 121 ilgsvlagmdldealgpnnsqhalakagletnslinieniansvktldfegqisqfsgkl 180
QY 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELNSLIENIANISVKTLDfEGQISQFGSKL 180
Db 181 qniklgltgdklnigglidkagldvisgllsgataalvldknastakkvagafela 240
QY 181 QNIKLGLTGDKLNIGGLDKAGLDVTSGLLSGATAALVLDKNASTAKKVAGAFELA 240
Db 241 ngvvgnitkavssylaqrvaaaglstgtpvaalvastvslaisplafagiadkfnhaskl 300
QY 241 NOVVGNITKAVSSYILAQRVAAGLSSTGTPVAALIASTVSLAISPLAFAGIADKFNHASKL 300
Db 301 esyaerfkklygdgnllaeaygrgtidasvtaintalaaiaaggvsaaagsviaspia 360
QY 301 ESYAERFKKLYGDGNLLAEYGRGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
Db 361 llvsgitgvtistilqyskqamfehvankihnkiveweknnhgnknyfengydarylanlqd 420
QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYLANLQD 420
Db 421 nmkflnlmkqlaerviaitqggwdnnigdlagrlsrlgekvlsqkayvdafesgkhika 480
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGLSRLGEKVLSGKAYVDAFEEGKHika 480
Db 481 dklvqldsangliidvsnsgkaktqhilfrtlltpgttghervvtgkyeytklinrnvd 540
QY 481 DKLVQDLSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRRVQTGKYEYITKLINRNVD 540
Db 541 swkltidgaasftdltnvvqrigieldnagnvttkettiaklgeddnnvfvsqgttei 600
QY 541 SWKITDGAASFTDLTNVVQRIEldNAGNVTKETKIIAKLGEGDNNVFVSGGTTEI 600
Db 601 dggegydrvhysrgnygaltidatketegsytnrvfvetgkalhevtsthtalvgnree 660
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETECSYTNRVFVETGKALHEVTSHTALVGNREE 660
Db 661 kleyrhnnqhagyytkdtklaveeiqtshndifkgskfndafnggdvtdiagnn 720
QY 661 KLEYRHNNQHAGYYTKDTLKAVEEIQTSNDIFKGSKFNDAFNGGDVTDIGNGN 720
Db 721 drlfgkgddiildgngddfidgkgndllhggkgddifvhrkgdndiitdsdgnkls 780
QY 721 DRLFCKGKDDILLDGGNDPFDGGKGNLHGGKGGDIFVHRKGGDNDIITDSGNDKLS 780
Db 781 fdsnlkldltfckvhnvltnskkevtiqnwfreadfakvppnykatkdekieleiigq 840
QY 781 FSDSNLKDLTFCKVHNVLTNSSKKEVTKQNWFEADPAKEVPNYKATKDEKIEEIIQ 840
Db 841 ngeritskvaddliakngkiktdelskvdyneyllkshknvtnslidkklissvsftasn 900
QY 841 NGERITSKVQDDLIKAGNGKIKITODELSKVVDNYELLKSHKNVTNSLDKLISSVSFTASN 900
Db 901 dgrnvlvaptmldgsslsqfar 924
QY 901 DSRNVLVAPTMLDQSSLSQFAR 924
RESULT 10
ID R42385 standard; Protein; 924 AA.
AC R42385;
DT 19-APR-1994 (first entry)
DE Recombinant leukotoxin peptide from plasmid pCR28.
KW Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
KW thromboembolic meningococcalitis; septicemia; arthritis;
KW pneumonia; lktA gene; haemin-binding protein; fusion protein.
OS Pasteurella haemolytica.
PN W09321323-A.
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PD 28-OCT-1993.
PF 05-APR-1993; CA0135.
PR 09-APR-1992; US-865050.
PR 04-JUN-1992; US-893424.
PR 04-JUN-1992; US-893426.
PR 29-MAR-1993; US-038287.
PR 29-MAR-1993; US-038288.
PR 29-MAR-1993; US-038719.
PA (UYSA-) UNIV SASKATCHEWAN.
PI Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
PI Rioux C, Theisen M;
DR WPI: 93-351733/44.
DR N-PSDB; Q51086.
PT Haemophilus somnus immunogenic proteins used in vaccines -
PT selected from haemin-binding protein, haemolysin, LppB and LppC,
PT and corresp. DNA
PS Disclosure: Fig 11; 119pp; English.
CC The lppB gene protein was expressed in E. coli as a fusion to the
CC pasteurella haemolytica leukotoxin gene lktA coded for by plasmid
CC pAA352. The lppB gene fragment was taken from pMS11. LppB can be
CC used in vaccines for preventing or treating H. somnus infections,
CC which cause thromboembolic meningococcalitis, septicemia, arthritis
CC and pneumonia in vertebrates.
CC See also R42370-86.
SQ Sequence 924 AA;
```

```
Query Match 98.4%; Score 6117; DB 8; Length 924;
Best Local Similarity 100.0%; Pred. NO. 0.00e+00;
Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


PT comprises chimeric protein comprising leuco:toxin peptide or
PT homologous protein fused to antigen esp. somatostatin or
PS gonadotropin releasing hormone
PS Example 2; Fig 6; 95pp; English.
CC Oligonucleotides contg. sequences from bovine somatostatin (SRIF)
CC gene were constructed on a Pharmacia Gene Assembler using standard
CC phosphoramidite chemistry. The oligonucleotides were annealed and
CC ligated into vector pAA352 (contg. the Pateurella haemolytica leuko-
CC toxin gene) which had been digested with BamHI. The ligated DNA was
CC used to transform E. coli strain JM105. Transformants contg. the
CC oligonucleotide inserts were identified by restriction endonuclease
CC mapping and the recombinant plasmid designated pAA496. The
CC chimeric protein produced from the plasmid works to bring about a
CC larger immune response than the antigen alone, i.e. the leukotoxin
CC works as a carrier protein.
CC See also R34545-8.
SQ Sequence 943 AA;

Query Match 98.2%; Score 6107; DB 7; Length 943;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 924; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 matvidlsfpgtgaakliilypqnydyteqngldgdkvkaaeelgievqreernniata 60
|||||
QY 1 MATVIDLSFPKTGAKKILILYPQNYDYTEQNGLDLVKAAEELGIEVQREERNNIATA 60
|||||

Db 61 qtslgtigtatgltgtergvlslapqldkllqktkagalsaesivqnankaktvlsqigs 120
|||||
QY 61 QTSLGTIQTATGLTGERGIVLSAPQIDKLLQKTAKGALGSAESIVQNANKAKTVLSGIQS 120
|||||

Db 121 ilgsvlagmdldealnqnsqhalakageltntslentiansvktldexceqisqfsgkl 180
|||||
QY 121 ILGSLVLAGMDLDEALQNNQHALAKAGELTNSLIENTIANSVKTLDFEGEIQSFGSKL 180
|||||

Db 181 qniklgltgdklnigglidraglgldvisgataalvldknastakvvgagfela 240
|||||
QY 181 QNIKLGTLGDKLNIGGLIDRAGLGLDVLSGLSGATALLVLDKNASTAKVVGAGFELA 240
|||||

Db 241 nqvvgntkavssyilaqrvaaglsstgtpvaaliaastvslaisplafagidkfnhaks 300
|||||
QY 241 NQVVGNTKAVSSYILAQRVAAGLSSTGTPVAALIASTVSLAISPLAFAGIDKFNHAKSL 300
|||||

Db 301 esvaerfkklgldgndlnaeyrgtqtidasvtaintalaaagvsaagsvlasplia 360
|||||
QY 301 ESTAEFRKKLGDGNDLNAEYRGTTQIDASVTAINALAAAGVSAAGSVLIASPLIA 360
|||||

Db 361 llvsgitgvtistilqyskqamfehvankihnkiveknhgknyfengydarylanlqd 420
|||||
QY 361 LLVSGITGVTISTILQYSKQAMFEHVANKIHNKIVEKNNHGKNYFENCYDARYLANLQD 420
|||||

Db 421 nmkflnlhnlkelaeraiatqgqwdnnlgdlagtsrlgkvlsgkayvdafeegkhika 480
|||||
QY 421 NMKFLNLNLKELAEARAIATQOQWDDNIGDLAGISRLGKVLGKAYVDAFEEGKHICA 480
|||||

Db 481 dklvqlidsangliidvnsqaktqthilfrtlltpotehrervqtgkyetklninrvd 540
|||||
QY 481 DKLVDQSDANGLIIDVNSQAKTQHILFRTPLLTPOTEHRERVQTGKYETKLNINRVD 540
|||||

Db 541 swkitdgaasstfdlnvvqrigielidnagnvktketkilaiklgegdndvfvgsattai 600
|||||
QY 541 SMKIIDGAASSTFDLNVVQRIIGIELDNAGNVKTKETKILAKLGESDNDVFGSGTTAI 600
|||||

Db 601 dggegydrvhysrgnygalatidatketegsytvnrftvetgkalhevtsthalvgnree 660
|||||
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHALVGNREE 660
|||||

Db 661 kleyrhnsnqhagyyktatlkaveiigtshndifkgskfdaifnggvgvdtidngdn 720
|||||
QY 661 KLEYRHNSNQHAGYYKTATLKAVEIIGTSHNDIFPKSKFADFNGGVGVDITDNGDN 720
|||||

Db 721 drlfgkgddildggngddfidgkgkndllhggkgddifvhrkgdndiitdsdgnakls 780
|||||
QY 721 DRLFGKGDDILDGGNGDDFIDGKGKNDLLHGGKGDDIFVHRKGDNDIITDSGDNKLS 780
|||||

Db 781 fsdsnlkdlitfekvkhnlvitnsskkekvtignwfreadafeakvpykatkdkeleeliqg 840
|||||
QY 781 FSDSNLKLDTTEKVKHNLVITNSKKEKVTIGNWFREADFAKEVPYKATKDEKIEEIIQ 840
|||||

Db 841 ngeritsqvadllakngkltqdekskvndnyellkshknvtalsldkllsvsaftsn 900
|||||
QY 841 NGERITSQVDDLIANGKKTQDELSKVNDNYELLKSHKNVTNSLDKLLSVSAFTSSN 900
|||||

Db 901 dsrnvlvaptmldgslslsfaras 926
|||||
QY 901 DSRNVLVAPTSMLDQSLSLSFARQS 926
|||||

RESULT 13
ID R34548 standard; Protein: 951 AA.
AC R34548;
DT 23-AUG-1993 (first entry)
DE Rotavirus VP4-leukotoxin gene fusion prod.
KW Vector: LKT 352; flanking; recombinant; antigen; somatostatin;
KW gonadotropin releasing hormone; rotavirus viral protein 4;
KW carrier protein; lactation; reproduction; SRIF.
OS Synthetic.
FH Key Location/Qualifiers
FT Protein 1..926
FT /note= "recombinant leukotoxin protein"
FT peptide 927..951
FT /note= "Rotavirus VP-4"
PN WO9308290-A.
PD 29-APR-1993.
PF 15-OCT-1992; CA0449.
PR 16-OCT-1991; US-779171.
PR 14-OCT-1992; US-960932.
PI (UYSA-) UNIV SASKATCHEWAN.
PA Hughes HPA, Potter AA, Redmond MJ;
DR WPI: 93-152482/18.
DR N-FSDB: Q41322.
PT Immunological carrier system with enhanced immunogenicity -
PT comprises chimeric protein comprising leuco:toxin peptide or
PT homologous protein fused to antigen esp. somatostatin or
PT gonadotropin releasing hormone
PS Example 2; Fig 8; 95pp; English.
CC Oligonucleotides contg. sequences from bovine Rotavirus viral
CC protein 4 (VP-4) gene were constructed on a Pharmacia Gene
CC Assembler using standard phosphoramidite chemistry. The oligo-
CC nucleotides were annealed and ligated into vector pAA352 (contg.
CC the Pateurella haemolytica leuko-toxin gene) which had been digested
CC with BamHI. The ligated DNA was used to transform E. coli strain
CC MH3000. Transformants contg. the oligonucleotide inserts were
CC identified by restriction endonuclease mapping and the recombinant
CC plasmid designated pAA501. The chimeric protein produced from the
CC plasmid works to bring about a larger immune response than the antigen
CC alone, i.e. the leukotoxin works as a carrier protein.
CC See also R34545-7.
SQ Sequence 951 AA;

Query Match 98.1%; Score 6100; DB 7; Length 951;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 923; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 matvidlsfpgtgaakliilypqnydyteqngldlvkaaeelgievqreernniata 60
|||||
QY 1 MATVIDLSFPKTGAKKILILYPQNYDYTEQNGLDLVKAAEELGIEVQREERNNIATA 60
|||||

Db 61 qtslgtigtatgltgtergvlslapqldkllqktkagalsaesivqnankaktvlsqigs 120
|||||
QY 61 QTSLGTIQTATGLTGERGIVLSAPQIDKLLQKTAKGALGSAESIVQNANKAKTVLSGIQS 120
|||||

Db 121 ilgsvlagmdldealnqnsqhalakageltntslentiansvktldexceqisqfsgkl 180
|||||
QY 121 ILGSLVLAGMDLDEALQNNQHALAKAGELTNSLIENTIANSVKTLDFEGEIQSFGSKL 180
|||||

Db 181 qniklgltgdklnigglidraglgldvisgataalvldknastakvvgagfela 240
|||||

QY 901 DSRNVLVAPTSMLDQSLSLQFARGS 926
|||||

RESULT 15

ID W13866 standard; Protein; 1098 AA.
AC W13866;
DT 12-MAY-1997 (first entry)
DE Chimeric protein #1.
KW RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine;
KW interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;
KW Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
KW fibrous pneumonia; cattle; therapy.
OS Synthetic.
PN US594107-A.
PD 14-JAN-1997.
PF 22-AUG-1990; 571301.
PR 22-AUG-1990; US-571301.
PR 16-OCT-1991; US-777715.
PR 20-DEC-1993; US-170126.
PA (CIBA) CIBA GEIGY CANADA LTD.
PA. (UYSA-) UNIV SASKATCHEWAN.
PI Campos M, Hughes HPA, Potter A;
DR WPI; 97-095929/09.
DR N-PSDB; T60032.
PT Immunogenic chimeric proteins comprising cytokine linked to RTX
PT toxin - useful in vaccines, esp. against shipping fever in cattle.
PS Claim 10; Column 25-32; 56pp; English.
CC W13866 and W13867 represent immunogenic chimeric proteins of the
CC invention. This sequence represents a chimeric protein containing the
CC bovine interleukin-2 (IL-2) sequence and a leukotoxin sequence. The
CC chimeric proteins of the invention comprise a cytokine, selected from
CC IL-2 and gamma interferon (gamma IFN), linked to at least one RTX toxin
CC epitope (preferably the sequence shown in W13865). The RTX toxin used to
CC provide the epitope sequence is preferably a leukotoxin, especially the
CC full-length Pasteurella haemolytica leukotoxin. Alternatively, the
CC leukotoxin is a truncated leukotoxin lacking leukotoxic activity,
CC especially LKT352. The chimeric proteins can be used for the production
CC of vaccines against respiratory diseases such as pneumonia, particularly
CC fibrinous pneumonia caused by P.haemolytica, including shipping fever in
CC cattle.
SQ Sequence 1098 AA:

Query Match 97.4%; Score 6057; DB 21; Length 1098;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 183 ktgakkilypqnyqdyteggnglqdvkaeeelgievqreernniatagtslgtqta 242
QY 11 KTGAKKILYIPQNYQDYTEGGNGLDLVKAAEELGIEVQREERNNIATAGTSLGTIOTA 70
Db 243 igltergivlsapqdkllqtkagaglsaesivqnankaktvlsigilgsvlagmd 302
QY 71 IGLTERGIVLSAPQDKLLQTKAGAGLSAESIVONANKAKTVLSIGIILGSLVAGMD 130
Db 303 idealqnsnhalakagleitnslieniansvktldfegedqisqfsgsklnikglgtlg 362
QY 131 LDEALQNSNQHAKAGLEITNSLIENIANSVKTLDFEGEQISQFGSKLQNIKRLGLTGL 190
Db 363 dklknigglkagldgvisgllsgataalvldknastakkvagfelanqvgvgnitka 422
QY 191 DKLKNIGGLDRAGLGDVLSGLLSGATLAALVLDKNASTAKKVAGFELANQVGNITKA 250
Db 423 vssyilagrvaaglsstgvpvaalvastvslaisplafagiadkfnhakslesyaerfkl 482
QY 251 VSSYILAQ RVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLESYAERFKL 310
Db 483 gydgnllaeayqrqgtgtidasvtaintalaaagvsaaagsviaspiallvsgitgvi 542
QY 311 GYDGNLLAEYQRGTGTIDASVTAINALAAAGVSAAAAGSVIASPIALLVSGITGVI 370
Db 543 stilgysqamfehvankihkiveeknnhgnknyfengydarylanlqdmkflnlknk 602
|||||

QY 371 STILOYSQAMFEHVANKIHNKIVEEKNHNGKNYFENGDYARYLANLQDMKFLNLNK 430
Db 603 elqaerviaitqgqwdnnigdlagisrlgekvlsqgkeyvdafaeegkhikadklvqlgsan 662
QY 431 ELQAERVIAITQQQWDDNNIGDLAGISRLGEKVLGSKAYVDFAFEGKHAKADKLVLQDSAN 490
Db 663 giidvsnsgaktqhilfrptllcpgtehrervqtgkyeyitklninrvdswkltddaas 722
QY 491 GIIDVSNSGAKTQHILFRPTLLTPGTEHREVRVQTGKYEYITKLNINRVDSWKITDGAAS 550
Db 723 stfdltvsvrgigleldnagnvktketkiaklgegdndvfvsggtteidggeggyrvh 782
QY 551 STFDLTVSVVRGIGLELDNAGNVKTKETKIAKLGEGDDNVFVSGSGTTEIDGEGGYDRVH 610
Db 783 ysrgnygaltidatketeggsyvtvnrfvetgkalhevtsthtalvgnreekieyrvhannq 842
QY 611 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRVHNNQ 670
Db 843 hhagyytkdtlkaveeeligtsndifkgskfndafnggdgvdtdidngdndrflfgkgdd 902
QY 671 HHAGYTTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGDGVDTDIDNGDNDRLFGKGDD 730
Db 903 ildegngddfidgkgkgnllhggkgddifvhrkgdgnidiitdsdgncklsfsgsnlkdl 962
QY 731 ILDEGNGDDFIDGKGNDLLHGGKGDDIFVHRKGDDNDIITDSGNDKLSFSDSNLKDLT 790
Db 963 fekvkhnlvitnsskkekvtlgnwfreadfakvnpnykatkdekleeeligngeritskv 1022
QY 791 FEKVKNLVITNSSKKEKVTIQNWFREADFAPVNPYKATKDEKIEEIIQNGERITSQV 850
Db 1023 ddliakngkitqdelakvvdnyellkhsknvtnsldklssvsaftssndsrnlvapt 1082
QY 851 DDLIKAGNGKITQDELSKVVDNYELLKHKSNVTNSLDKLSSVSFAFTSSNDSRNLVAPT 910
Db 1083 smldqslssllqfargs 1098
QY 911 SMLDQSLSSLLQFARGS 926

Search completed: Wed Dec 9 19:19:58 1998
Job time : 242 secs.

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:20:16 1998; MasPar time 33.89 Seconds
Tabular output not generated. 942.937 Million cell updates/sec

Title: >US-08-455-970-12
Description: (1-936) from US08455970.pep
Perfect Score: 6217
Sequence: 1 MATVIDLSFPKTKAKKIILY.....LSSLOFARGSQHWSYGLRPG 936

Scoring table: PAM 150
Gap 11

Searched: 107076 seqs, 34141958 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 55.004; Variance 163.629; scale 0.336

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6037	97.1	953	1	B30169 leukotoxin A - Pasteu	0.00e+00
2	5510	88.6	955	1	A35254 leukotoxin A - Pasteu	0.00e+00
3	4254	68.4	956	1	B33389 toxin II - Actinobaci	0.00e+00
4	4198	67.5	956	1	A43834 toxin II - Actinobaci	0.00e+00
5	2616	42.1	1052	1	B49219 toxin III - Actinobac	0.00e+00
6	2566	41.3	1049	1	S51784 toxin III - Actinobac	0.00e+00
7	2398	38.6	1023	1	LECA hemolysin A - Escheri	0.00e+00
8	2385	38.4	1024	2	S10056 hemolysin A - Escheri	0.00e+00
9	2321	37.3	998	2	I41078 hemolysin - Escherich	4.17e-299
10	2291	36.9	1022	1	I39643 RTX-toxin I - Actinob	7.96e-295
11	2207	35.5	1055	1	A37205 leukotoxin A - Actino	7.59e-283
12	1208	19.4	208	2	S34238 leukotoxin A - Pasteu	1.43e-141
13	896	14.4	1705	1	OYBRC cyclolysin - Bordetel	2.76e-98
14	887	14.3	1706	2	S51672 adenylate cyclase hem	4.77e-97
15	286	4.6	1829	2	S35027 cytotoxin RTX homolo	7.59e-18
16	265	4.3	1115	2	A47058 Fe-regulated RTX cyto	2.37e-15
17	221	3.6	835	2	JC6140 cell surface-associat	2.75e-10
18	224	3.6	991	2	I39739 mannuronan C5 epimer	1.27e-10
19	217	3.5	597	2	S74999 iron-regulated protei	7.71e-10
20	203	3.3	1741	2	S74910 hemolysin - Synchocy	2.71e-08
21	187	3.0	476	2	A43942 lipase - Pseudomonas	1.44e-06
22	173	2.8	284	2	S98385 nod protein - Rhizob	4.21e-05
23	173	2.8	284	2	A43721 nodule formation prot	4.21e-05

24	165	2.7	475	2	S48132 metalloproteinase G (2.76e-04
25	166	2.7	479	2	A38307 metalloproteinase C (2.19e-04
26	170	2.7	481	2	A33712 metalloproteinase B (8.55e-05
27	169	2.7	1771	2	S76851 hypothetical protein	1.08e-04
28	164	2.6	472	2	A30160 metalloproteinase (EC	3.48e-04
29	162	2.6	478	2	A36137 metalloproteinase (EC	5.53e-04
30	160	2.6	613	2	JS0763 triacylglycerol lipas	8.77e-04
31	164	2.6	1290	2	S76853 hypothetical protein	3.48e-04
32	159	2.6	3591	2	S10236 filamentous hemagglut	1.10e-03
33	159	2.6	3591	2	S21010 filamentous hemagglut	1.10e-03
34	156	2.5	476	2	A41463 alkaline metalloprote	2.19e-03
35	154	2.5	478	2	JN0892 metalloproteinase (EC	3.44e-03
36	152	2.4	449	2	JO1277 triacylglycerol lipas	5.39e-03
37	150	2.4	479	2	S26699 alkaline proteinase -	8.43e-03
38	147	2.4	504	2	S12164 metalloproteinase (EC	1.64e-02
39	150	2.4	3016	2	S77300 hypothetical protein	8.43e-03
40	145	2.3	479	2	JN0891 metalloproteinase (EC	2.54e-02
41	137	2.2	1574	1	A38454 myosin MYO2 - yeast (1.43e-01
42	134	2.2	2035	2	A56088 host cell factor Cl p	2.70e-01
43	133	2.1	550	2	A28166 Kupffer cell receptor	3.32e-01
44	133	2.1	1959	1	A33977 myosin heavy chain, n	3.32e-01
45	133	2.1	2035	2	A40718 host cell factor C1 p	3.32e-01

ALIGNMENTS

RESULT 1

ENTRY B30169 #type complete
TITLE leukotoxin A - Pasteurella haemolytica (serotype 1)
ALTERNATE_NAMES lktA protein
ORGANISM #formal_name Pasteurella haemolytica
DATE 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 05-Sep-1997

ACCESSIONS B30169; C32051; S29516
REFERENCE A30169
#authors Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
#journal DNA (1989) 8:15-28
#title DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.

#cross-references MUID:89210283
#accession B30169
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-953 ##label HIG

REFERENCE A32051
#authors Strathdee, C.A.; R.Y.C.
#journal J. Bacteriol. (1989) 71:916-928
#title Cloning, nucleotide sequence, and characterization of genes encoding the secretion function of the Pasteurella haemolytica leukotoxin determinant.

#cross-references MUID:89123172
#accession C32051
#status not compared with conceptual translation
#molecule_type DNA
#residues 947-953 ##label STR

REFERENCE S29515
#authors Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
#journal Infect. Immun. (1987) 55:1987-1996
#title Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica A1.

#accession S29516
#molecule_type DNA
#residues 1-741, 'p', 743-953 ##label LOR
#cross-references EMBL:M20730; NID:g150492; PID:g150494

COMMENT This organism causes bovine pneumonic pasteurellosis (shipping fever).

GENETICS
#gene lktA
#description lyses leukocytes
CLASSIFICATION #superfamily hemolysin A; hemolysin A homology
KEYWORDS calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;

tandem repeat

```

FEATURE
238-784      #domain hemolysin A homology #label HLXA\
716-807      #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)\
716-724      #region repeat #status atypical\
725-733      #region repeat #status atypical\
734-742      #region repeat\
743-751      #region repeat\
752-760      #region repeat\
761-769      #region repeat\
770-778      #region repeat\
779-787      #region repeat\
790-798      #region repeat\
799-807      #region repeat\
554          #binding_site palmitate (Lys) (covalent) #status
              predicted
SUMMARY      #length 953 #molecular-weight 102044 #checksum 6834
              97.1%; Score 6037; DB 1; Length 953;
Query Match  Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 913; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 38 KTGAKKILYIPQNYQDYDEQNGLDLVKAAEELGIEVQREERNNIATAQSLGTIQT 97
QY 11 KTGAKKILYIPQNYQDYDEQNGLDLVKAAEELGIEVQREERNNIATAQSLGTIQT 70
Db 98 IGLTERGIVLSAPOIDKLQKTKAGQALGSAESIVQNANKAKTVLSGIQSLGVLGMD 157
QY 71 IGLTERGIVLSAPOIDKLQKTKAGQALGSAESIVQNANKAKTVLSGIQSLGVLGMD 130
Db 158 LDEALQNNQHALAKAGLELTNSLTENTANSVKTIDFEGEQISQFGSKLQNKIGLGTIG 217
QY 131 LDEALQNNQHALAKAGLELTNSLTENTANSVKTIDFEGEQISQFGSKLQNKIGLGTIG 190
Db 218 DLKLTGGLDKAGLDVLSGLSGATAALVADKNASTAKKVGAGFELANOVVGNITRA 277
QY 191 DLKLTGGLDKAGLDVLSGLSGATAALVADKNASTAKKVGAGFELANOVVGNITRA 250
Db 278 VSSYILAQRVAAGLSSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESAERFKKL 337
QY 251 VSSYILAQRVAAGLSSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESAERFKKL 310
Db 338 GYDGNLLAEYQRTGCTIDASVTAINALAAIAGGVSAAGSVIASPALLVSGITGVI 397
QY 311 GYDGNLLAEYQRTGCTIDASVTAINALAAIAGGVSAAGSVIASPALLVSGITGVI 370
Db 398 STILOYSKOAMFEHVANKIHNVKHNHKNYFENGVDARYLANLODNKFFLLNLNK 457
QY 371 STILOYSKOAMFEHVANKIHNVKHNHKNYFENGVDARYLANLODNKFFLLNLNK 430
Db 458 ELQARVIAITQOQWNNIGDLAGISRLGKELVSGKAYVDAFEEGKHAKDLVQLDSAN 517
QY 431 ELQARVIAITQOQWNNIGDLAGISRLGKELVSGKAYVDAFEEGKHAKDLVQLDSAN 490
Db 518 GIIDVNSGKAKTQHILFRLPTLTPTGTEHRRVQTGKYEYITKLNINRVDSWKITDGAAS 577
QY 491 GIIDVNSGKAKTQHILFRLPTLTPTGTEHRRVQTGKYEYITKLNINRVDSWKITDGAAS 550
Db 578 STFDLNVVQRIEGLDNAGNVTKTKETKIIAKLGLGDDNVFVSGTTEIDGEGYDRVH 637
QY 551 STFDLNVVQRIEGLDNAGNVTKTKETKIIAKLGLGDDNVFVSGTTEIDGEGYDRVH 610
Db 638 YSRGNYGALTIDATKETECSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 697
QY 611 YSRGNYGALTIDATKETECSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 670
Db 698 HHAGYTKDTLKAVEELIGTSHNDIFPKSGFNDAFNGGVDVTIYNDGNDRLFGGKGD 757
QY 671 HHAGYTKDTLKAVEELIGTSHNDIFPKSGFNDAFNGGVDVTIYNDGNDRLFGGKGD 730
Db 758 ILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDT 817
QY 731 ILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDT 790

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Db 818 FEKVHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEEIQNGERITSKQV 877
QY 791 FEKVHNLVITNSKKEKVTIQNWFRADFAKEVPYKATKDEKIEEIQNGERITSKQV 850
Db 878 DDLIAKGNGKITQDELISKVDVYELLKHKSNVTSLDKLISVSFAFTSSNDSRNVLVAPT 937
QY 851 DDLIAKGNGKITQDELISKVDVYELLKHKSNVTSLDKLISVSFAFTSSNDSRNVLVAPT 910
Db 938 SMLDQSLSLQFARAA 953
QY 911 SMLDQSLSLQFARGS 926

RESULT 2
ENTRY   A35254      #type complete
TITLE   leukotoxin A - Pasteurella haemolytica (serotype T10)
ALTERNATE_NAMES
ORGANISM lktA protein
FORMAL_NAME Pasteurella haemolytica
DATE     10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change
         05-Sep-1997
ACCESSIONS
REFERENCE S37145; A35254; S34237; S34235
#authors Lainson, A.F.; Aitchison, K.; Donachie, W.
#submission submitted to the EMBL Data Library, September 1993
#description DNA sequence of the leukotoxin A gene from P. haemolytica T10
          serotype.
#accession S37145
#molecule_type DNA
#residues 1-955 #label LA1
#cross-references EMBL:226247; PID:g400425
REFERENCE A35254
#authors Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
#journal J. Bacteriol. (1990) 172:2343-2350
#title Secretion and expression of the Pasteurella haemolytica
          leukotoxin.
#cross-references MUID:90236888
#accession A35254
#status preliminary
#molecule_type DNA
#residues 950-955 #label HIG
#cross-references GB:M24197; GB:M34943; GB:M34944
REFERENCE S34235
#authors Lainson, A.F.; Aitchison, K.D.; Donachie, W.
#submission submitted to the EMBL Data Library, June 1993
#description DNA sequence of the carboxy terminal end of leukotoxin A from
          the T3 serotype of Pasteurella haemolytica.
#accession S34237
#molecule_type DNA
#residues 745-955 #label LA2
#cross-references EMBL:22884; PID:g311829
#experimental_source serotype T3
#accession S34235
#molecule_type DNA
#residues 723-955 #label LA3
#cross-references EMBL:22887; PID:g311824; PID:g311825
#experimental_source serotype T10

FUNCTION
#description attacks cell membranes and causes cell lysis
CLASSIFICATION #superfamily hemolysin A; hemolysin A homology
KEYWORDS        calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
               tandem repeat

FEATURE
240-786      #domain hemolysin A homology #label HLXA\
718-809      #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)\
718-726      #region repeat\
727-735      #region repeat\
736-744      #region repeat\
745-753      #region repeat\
754-762      #region repeat\
763-771      #region repeat\
772-780      #region repeat\
781-789

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792-800      #region repeat\
801-809      #region repeat\
556          #binding_site palmitate (Lys) (covalent) #status
SUMMARY      #length 955 #molecular-weight 102187 #checksum 4735
Query Match   88.6%; Score 5510; DB 1; Length 955;
Best Local Similarity 88.4%; Pred. No. 0.00e+00;
Matches 810; Conservative 60; Mismatches 46; Indels 0; Gaps 0;

Db 40 KNGAKIILYIPKDYKSGNGQLDLVKAEEGLGIEVQKEGNDIAKAQTSLSGTONV 99
QY 11 KTGAKIILYIPQNYQYDEQNGQLDLVKAEEGLGIEVQREERNIATAQTSLSGTO 70
Db 100 LGLTERGIVLSAPQDKLLQKNVQALGSSESTAQNTSVQAKTVLSGVQNSRTVL 159
QY 71 IGLTERGIVLSAPQDKLLQKNVQALGSSESTAQNTSVQAKTVLSGVQNSRTVL 130
Db 160 LDEALQNESDQLTLAKAGLELNSLIENANSVOTLDAFSEQISQFSGKLQNVKGL 219
QY 131 LDEALQNSNQHALAKAGLELNSLIENANSVKTLDGFEQISQFSGKLQNKIKGL 190
Db 220 DLKKNIGGLDKAGLDGDKVSRLLSGATAALVLDADAKTAKVAGFELANOVGNIT 279
QY 191 DLKKNIGGLDKAGLDGDKVSRLLSGATAALVLDADAKTAKVAGFELANOVGNIT 250
Db 280 VSSYILAORVAAGLSTGTPVAALIASTVAIAISPLSFAGIADKFDRAKSLN 339
QY 251 VSSYILAORVAAGLSTGTPVAALIASTVAIAISPLSFAGIADKFDRAKSLN 310
Db 340 GYEGSLAEYOHGTGTIDASTVNTALAAATAGVSAAGSVASPTALVSGITGVI 399
QY 311 GYEGSLAEYOHGTGTIDASTVNTALAAATAGVSAAGSVASPTALVSGITGVI 370
Db 400 STILOYSKOAMEHVAHANKIHNKIVWEKNNGKNTFENGVDARYLANLDQNMK 459
QY 371 STILOYSKOAMEHVAHANKIHNKIVWEKNNGKNTFENGVDARYLANLDQNMK 430
Db 460 ELQAEVIAITQQQWDSNIGDLGASIRLGEKVLKSKAYVDAFEGQHLKADKL 519
QY 431 ELQAEVIAITQQQWDSNIGDLGASIRLGEKVLKSKAYVDAFEGQHLKADKL 490
Db 520 GIIDVTNTGEAKTOHLFTPLTPTGTEKREVRVQTKYEYITKLNINRVDSW 579
QY 491 GIIDVTNTGEAKTOHLFTPLTPTGTEKREVRVQTKYEYITKLNINRVDSW 550
Db 580 STFDLTNNVQRIGVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDG 639
QY 551 STFDLTNNVQRIGVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDG 610
Db 640 YSRGNYGALTIDATKETECSYTVNRVFSKALHEGTSHTALYGNREKIEYRH 699
QY 611 YSRGNYGALTIDATKETECSYTVNRVFSKALHEGTSHTALYGNREKIEYRH 670
Db 700 HHAGYTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDITDNGDNRFLFG 759
QY 671 HHAGYTKDTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDITDNGDNRFLFG 730
Db 760 IIDGGNGDDFIDGGKNDLHGGKGGDDIFVHRQGGDNDITSEGNDKLSFSD 819
QY 731 IIDGGNGDDFIDGGKNDLHGGKGGDDIFVHRQGGDNDITSEGNDKLSFSD 790
Db 820 FEKVNHLVITNTKQKVITQNWFEAEFAKTIQNTVATRDDEKIEIIGONGER 879
QY 791 FEKVNHLVITNTKQKVITQNWFEAEFAKTIQNTVATRDDEKIEIIGONGER 850
Db 880 DELIEKNGKIAQSELTQVNDVQYLLKYSRDSASNLKLISSAFTSSNDRNVL 939
QY 851 DDLIAKNGKITQDELKSKVDVNYELLKHSKNVTNSLDKLISVSAFTSSNDRN 910
Db 940 SMLDPSLSSIOFARAA 955
QY 911 SMLDPSLSSIOFARAA 926
```

```
RESULT 3
ENTRY
TITLE      #type complete
ALTERNATE_NAMES
ORGANISM   #formal name Actinobacillus pleuropneumoniae
DATE       #sequence-revision 01-Nov-1996 #text_change
06-Dec-1996
B33389     #accession
B33389     #residues 1-956 #label CHA
B33389     #cross-references GB:M30602; PID:g141825
B33389     #experimental_source serotype 5
B33389     #authors
          Smits, M.A.; Briare, J.; Jansen, R.; Smith, H.E.; Kamp,
          E.M.; Gielkens, A.L.J.
          submitted to the EMBL Data Library, July 1991
          Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
          #description
          #accession S18852
          #molecule_type DNA
          #residues 1-956 #label SWI
          #cross-references EMBL:X61111; PID:g38941
          A43599
          Smits, M.A.; Briare, J.; Jansen, R.; Smith, H.E.; Kamp,
          E.M.; Gielkens, A.L.J.
          Infect. Immun. (1991) 59:4497-4504
          Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
          #cross-references MUID:92040145
          #accession B43599
          #status preliminary
          #molecule_type DNA
          #residues 1-27:948-956 #label SM2
          #cross-references GB:X61111
          #comment This organism causes porcine pleuropneumonia.
          #genetics
          #gene
          #function
          #description
          #classification
          #keywords
          attacks blood cell membranes and causes cell lysis
          #superfamily hemolysin A; hemolysin A homology
          calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
          tandem repeat
          #domain hemolysin A homology #label HLVA\
          #region 9-residue repeats\
          #region repeat #status atypical\
          #region repeat #status atypical\
          #region repeat\
          #region repeat\
          #region repeat\
          #region repeat\
          #region repeat\
          #region repeat\
          #binding_site palmitate (Lys) (covalent) #status
          predicted
          #length 956 #molecular-weight 102531 #checksum 5232
SUMMARY
Query Match 68.4%; Score 4254; DB 1; Length 956;
Best Local Similarity 67.1%; Pred. No. 0.00e+00;
Matches 615; Conservative 155; Mismatches 139; Indels 8; Gaps 7;

Db 45 GAKKILYIPQY--DSGGNGVQDLVKAANDLGEVWEERSNLDIAKTSFDTQKILG 102
QY 13 GAKKILYIPQYQYDEQNGQLDLVKAEEGLGIEVQREERNIATAQTSLSGTO 72
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```
Db 103 FTRGIVLAPQDLNLLKKNPKIGNTLGSASSISQNIKANTVLTGGISQILGSLVSGVNL 162
Qy 73 LTERGIVLSAPQDKLQKT-KAGQALGSAESIVQNKAKTAVLGSQISILGSLVACMDL 131
Db 163 NELLQNDPNOLELAKAGLELTNELVGNIASSVQTVDAFAEQISKGLSHQNLVKGGLS 222
Qy 132 DEALQN-NSNQHALAKAGLELTNSLIENIANSVKTLDFEQEIQSQFSGKQNLKGLTIG 190
Db 223 NKQLNLPDLGKASGLDIIISGLLSGASAGLILADKEASTEKAAGVAFANQIIGNTKA 282
Qy 191 DKLKNIIGLDKAGLGLDVISGLLSGATAALVADKNASTAKVAGFELANQVVGNTKA 250
Db 283 VSSYILAQRVASGLSSGTPVAALIASTVALAVSPLSLNVADKFAEQADLKLSYERFQKL 342
Qy 251 VSSYILAQRVASGLSSGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLAESYERFQKL 310
Db 343 GYDGRLLADFHRETCTIDASVTNTALAAISGGVGAASAGSLVAGPALLVAGVTGLI 402
Qy 311 GYDGNLLAEYORGTGTIDASVTNTALAAISGGVGAASAGSLVAGPALLVAGVTGLI 370
Db 403 TTILEYSKOAMFEHVANKVHVRIVEK-KHNKYPEQGYDSRHLADLNQNMKFLNLNK 461
Qy 371 STILOYSKOAMFEHVANKVHVRIVEK-KHNKYPEQGYDSRHLADLNQNMKFLNLNK 430
Db 462 ELQAEVVAITQORWNOIGDLAAISRRTDKISSGKAYVDAFEBGQHSQYDSSVOLDNKN 521
Qy 431 ELQAEVVAITQOQWNNIGDLGSRGKLVSGKAYVDAFEBGKHAKDLVQLDSAN 490
Db 522 GIINISNTNR-KTQSVLFRTPPLTPGEEENRERIOEGKNSYITKLHIQRVDSVTTDGDAS 580
Qy 491 GIIDVNSGKAKTOHILFRTPPLTPGTEHREVRVQTKYEVITKLINRVDNWSKITDGAAS 550
Db 581 SSVDFTNVQREAVKFDAGNIIESKOTKIIANLGNAGNDNVFVGSSTVTDGGDGHDRVH 640
Qy 551 STFDLNVVQRIEILDNAGNVTKETKIIAKLGEEDNDNVFVGSSTVTDGGDGHDRVH 610
Db 641 YSRGEYALVDAETAEKGSYKRVYVQSKALHETIATHOTNVGNREKIEYRREDDR 700
Qy 611 YSRGNYGALITDAKTEQGSYTVNRVETGKALHEVTSHTLVLGNREKIEYRHSNQQ 670
Db 701 FHTGYTVTDSLKSVEEIIIGSFQDDIFKGSQFDDVFHGGNGVDTIDGNDGDHHLFGGAGGD 760
Qy 671 HHAGYVTKDLKAVEEIIIGTSHNDIFKGSQFDDVFHGGNGVDTIDGNDGNDLFLFGGKDD 730
Db 761 VIDGNGNDELVGCTGNDIISGGKNDIYVHKTDGNDSDITDGGQDKLAFSDVNLKDLT 820
Qy 731 ILDGGNGDDFDGKGKNDLHGGKDDIFVHRKGDNDIITDSDGNDKLSFSDSNLKDLT 790
Db 821 FKVDLSLEIINQKGVKRVGNWFEEDLASTVANYKATNDKITEEIIIGKGERITSEQV 880
Qy 791 FEKVHNLVITNSKKEVVTQNWFEADFAKEVPNYKATKDEKIEEIIIGQGERITSEQV 850
Db 881 DKLIEKGNQISAPALSKVVDNYNTSKDRQNVNSLAKLISVSGFSSTSSDFRNLGTYV 940
Qy 851 DDLIAKNGKITQDELKSVVDNYELLKHSKNTVNSLQKISVSAFTSSNDSRNLVA-P 909
Db 941 PSSIDVS-NNIQLARAA 956
Qy 910 TSMLDQSLSSIQFARGS 926
```

```
RESULT 4
ENTRY A43834 #type complete
TITLE toxin II - Actinobacillus suis
ALTERNATE_NAMES asha protein; cytotoxin II; RTX-toxin II
ORGANISM #formal_name Actinobacillus suis
DATE 31-Dec-1993 #sequence_revision 08-Nov-1996 #text_change
ACCESSIONS A43834
REFERENCE #authors Burrows, L.L.; Lo, R.Y.
#journal Infect. Immun. (1992) 60:2166-2173
#title Molecular characterization of an RTX toxin determinant from
```

```
#cross-references MUID:92267623
#accession A43834
#molecule_type DNA
##residues 1-956 ##label BUR
##experimental_source isolate 3714
##note sequence extracted from NCBI backbone (NCBIN:104212,
NCBIP:104211)
COMMENT This organism causes acute fatal septicemia in young pigs.
FUNCTION attacks cell membranes and causes cell lysis
#description #superfamily hemolysin A; hemolysin A homology
CLASSIFICATION calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
KEYWORDS tandem repeat
FEATURE
243-787 #domain hemolysin A homology #label HLYA\
719-801 #region 9-residue repeats\
719-727 #region repeat #status atypical\
728-736 #region repeat #status atypical\
737-745 #region repeat\
746-754 #region repeat\
755-763 #region repeat\
764-772 #region repeat\
773-781 #region repeat\
782-790 #region repeat\
793-801 #region repeat\
557 #binding_site palmitate (Lys) (covalent) #status
predicted
SUMMARY #length 956 #molecular-weight 102527 #checksum 5171
Query Match 67.5%; Score 4198; DB 1; Length 956;
Best Local Similarity 66.5%; Pred. No. 0.00e+00;
Matches 610; Conservative 155; Mismatches 144; Indels 8; Gaps 7;
Db 45 GAKKILYTPQGV--DSGGNGVQDLVKAANDLIGVWREERSNLDAKTSFDTTKILG 102
Qy 13 GAKKILYTPQVYQYDEQNGLDLVKADELGIEVQREERNIATQTSIGTQITAG 72
Db 103 FTRGIVLAPQDLNLLKKNPKIGNTLGSASSISQNIKANTVLTGGISQILGSLVSGVNL 162
Qy 73 LTERGIVLSAPQDKLQKT-KAGQALGSAESIVQNKAKTAVLGSQISILGSLVACMDL 131
Db 163 NELLQNDPNOLELAKAGLELTNELVGNIASSVQTVDAFAEQISKGLSHQNLVKGGLS 222
Qy 132 DEALQN-NSNQHALAKAGLELTNSLIENIANSVKTLDFEQEIQSQFSGKQNLKGLTIG 190
Db 223 NKQLNLPDLGKASGLDIIISGLLSGASAGLILADKEASTEKAAGVAFANQIIGNTKA 282
Qy 191 DKLKNIIGLDKAGLGLDVISGLLSGATAALVADKNASTAKVAGFELANQVVGNTKA 250
Db 283 VSSYILAQRVASGLSSGTPVAALIASTVALAVSPLSLNVADKFAEQADLKLSYERFQKL 342
Qy 251 VSSYILAQRVASGLSSGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLAESYERFQKL 310
Db 343 GYDGRLLADFHRETCTIDASVTNTALAAISGGVGAASAGSLVAGPALLVAGVTGLI 402
Qy 311 GYDGNLLAEYORGTGTIDASVTNTALAAISGGVGAASAGSLVAGPALLVAGVTGLI 370
Db 403 TTILEYSKOAMFEHVANKVHVRIVEK-KHNKYPEQGYDSRHLADLNQNMKFLNLNK 461
Qy 371 STILOYSKOAMFEHVANKVHVRIVEK-KHNKYPEQGYDSRHLADLNQNMKFLNLNK 430
Db 462 ELQAEVVAITQORWNOIGDLAAISRRTDKISSGKAYVDAFEBGQHSQYDSSVOLDNKN 521
Qy 431 ELQAEVVAITQOQWNNIGDLGSRGKLVSGKAYVDAFEBGKHAKDLVQLDSAN 490
Db 522 GIINISNTNR-KTQSVLFRTPPLTPGEEENRERIOEGKNSYITKLHIQRVDSVTTDGDAS 580
Qy 491 GIIDVNSGKAKTOHILFRTPPLTPGTEHREVRVQTKYEVITKLINRVDNWSKITDGAAS 550
Db 581 SSVDFTNVQREAVKFDAGNIIESKOTKIIANLGNAGNDNVFVGSSTVTDGGDGHDRVH 640
Qy 551 STFDLNVVQRIEILDNAGNVTKETKIIAKLGEEDNDNVFVGSSTVTDGGDGHDRVH 610
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QY 722 RLFGGKDDILDGGNGDDFDGKGKNDLLHGGKDDIFVHRKGDND 768

RESULT 6

ENTRY S51784 #type complete

TITLE toxin III - Actinobacillus pleuropneumoniae (serotype 2)

ALTERNATE_NAMES RTX-toxin IIIA (ApXIIIA)

ORGANISM #formal_name Actinobacillus pleuropneumoniae

DATE 14-Jul-1995 #sequence_revision 15-Nov-1996 #text_change 06-Dec-1996

ACCESSIONS S51784

REFERENCE S51783

#authors Chang, Y.F.; Shi, J.; Ma, D.P.; Shin, S.J.; Lein, D.H.

#journal DNA Cell Biol. (1993) 12:351-362

#title Molecular analysis of the Actinobacillus pleuropneumoniae RTX toxin-III gene cluster.

#accession S51784

#status preliminary

#molecule_type DNA

#residues 1-1049 #label CHA

#cross-references EMBL:L12145; FID:g470685

COMMENT This organism causes porcine pleuropneumonia.

GENETICS

#gene apXIIIA

FUNCTION

#description lyses lung macrophages

CLASSIFICATION #superfamily hemolysin A; hemolysin A homology

KEYWORDS calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat

FEATURE

254-803 #domain hemolysin A homology #label HLXA

735-861 #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYIF]-X)

735-743 #region repeat #status atypical

744-753 #region repeat #status atypical

753-761 #region repeat

762-770 #region repeat

771-779 #region repeat

780-788 #region repeat

789-797 #region repeat

798-806 #region repeat

807-815 #region repeat

817-825 #region repeat #status atypical

826-834 #region repeat

835-843 #region repeat

844-852 #region repeat

853-861 #region repeat

571,702 #binding_site palmitate (Lys) (covalent) #status predicted

SUMMARY

#length 1049 #molecular-weight 112491 #checksum 8565

Query Match 41.3%; Score 2566; DB 1; Length 1049;

Best Local Similarity 52.2%; Pred. No. 0.00e+00;

Matches 401; Conservative 177; Mismatches 167; Indels 23; Gaps 20;

Db 55 GNKLVLVIP-K-EYDGSVNGFEDLVKAAEELGIVQVYRNLEVAHSLGTAQFGL 112

QY 14 AKRIILIFQNTFYDEQNGQDLVKAABELGIEVQREERNIATAQ'LSLTQIATGL 73

Db 113 TERGLTFLAPQLDQFLQKHSKNVYVSGSTGDAVSLAKSQTIIISQIVLGTVLGINL 172

QY 74 TERGIVLSAPQIDKLLQK-TKAQALGSAES-IVQNANKATVLSQISILSVLAGMDL 131

Db 173 NEAITSGGSELEAEAGVSLAESLVNSIAKGTITIDAFQTQONFG-KLAENAKGLGGVG 231

QY 132 DEALQNNNQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL-QNIKGLGTIG 190

Db 232 ROLQNTSGSALSKTGLGLDIISLSLSGVTRSFALRNKNASTTKVAAGFELSNQVIGIT 291

QY 191 DKLNIKG--LQKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELANQVGNIT 248

Db 292 KAVSSYILAQRLRAGLSTTGPAALIASISLAISPLAFRLVADNFRNSKEIGEFARFK 351

QY 249 KAVSSYILAQRAAGLSSTGPAALIASISLAISPLAFAGIADNFHAKSLESIAERFK 308

Db 352 KLGYDGDKLLSEFYHEAGTIDASITTIISTALSAAGTAASAGALVGCAPITLLVTGITG 411

QY 309 KLGYDGDNLLAEYQGTCTIDASVTAINTAALAAAGGVSAAAGSVIASPIALLVSGITG 368

Db 412 LISGLEFSKPMLDHVASKIGNKIDWEKK-YGKNYFENGYDARHKAFLEDSESLSSF 470

QY 369 VISTLIQISKAMFEHVANKIHNKIVWEKNNHKNYFENGYDARYLANLQDNKKFLNL 428

Db 471 NKQYTERAVLITQQRWDEYIGELAGITGKGLSSGRAYVYDFQEGKLLKPKPDFSKV 530

QY 429 NKLQAEVIALITQQQWNNIGDLAGISRLGEKVLGRAYVDAFEKGHI--KADKL--V 484

Db 531 VDPYTKGIDISNS-OTSTL-LKFVTPLLTPTGTSRERTQTKYEYITKLVKVGKDKWV 588

QY 485 QLDSSANGIIDSNSGKAKTQHLFTPLLTPTGTEHREVRVQTKYEYITKLINRVDSWKI 544

Db 589 NGVKDKGAVDYTNLIQAHIS--SSVARGEYREVRVLSHLGNGNDKVFLAAGSAEIHAG 647

QY 545 TDGAA-SSTFDLTNNVQIRIGIELDNAGNVTKETKIILAKIGEGDNNVFGSGTTEIDGG 603

Db 648 EGHVYVYDKTDGTLIVIDGKATEQGRYSVTRLSGATKILREVKNQKAVGKREETL 707

QY 604 EGYDRVHYSRNGYALTIDATKETEQGSYTVNR-FVETGKALHEVTSHTALVGNREKI 662

Db 708 EYRDYELTQSGNSNLKAHDELHVSVEEI-GSNORDEFKSGKFRDIFHGADGDDLLNGNDG 766

QY 663 EYRHSN-NQH-HAGYTTKDTLKAVEEIIIGTSHNDIFKSGKFNDAFNGGVDVTIDGNDG 720

Db 767 DILYDCKGNDELRGDNDOLYGGEGDDKLLGGGNN-YL-SGGDGDND 812

QY 721 DRLFQGGKDDILDGGNGDDFDGKGKNDLLHGGKDDIFVHRKGDND 768

RESULT 7

ENTRY LEECA #type complete

TITLE hemolysin A - Escherichia coli

ORGANISM #formal_name Escherichia coli

DATE 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 20-Mar-1998

ACCESSIONS A24433; I41280

REFERENCE A24433

#authors Felmlee, T.; Pellett, S.; Welch, R.A.

#journal J. Bacteriol. (1985) 163:94-105

#title Nucleotide sequence of an Escherichia coli chromosomal hemolysin.

#cross-references MUID:85234404

#accession A24433

#molecule_type DNA

#residues 1-1023 #label FEL

#cross-references GB:M10133; GB:M12863; NID:g146377; PID:g146379

#experimental_source strain J96, O4 serotype

REFERENCE A55387

#authors Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.

#journal Science (1994) 266:1992-1996

#title Fatty acylation of two internal lysine residues required for the toxic activity of Escherichia coli hemolysin.

#note annotation; lysine palmitoylation

#contents lysine modification is performed by the hlyC gene product

REFERENCE I41280

#authors Haertlein, M.; Schiessl, S.; Wagner, W.; Rdest, U.; Kreft, J.; Goebel, W.

#journal J. Cell Biol. (1983) 22:87-97

#title Transport of hemolysin by Escherichia coli.

#accession I41280

#status translated from GB/EMBL/DBJ

#molecule_type DNA

#residues 1,T',3,V',5,T',7-44 #label RES

#cross-references GB:M29173; NID:g146337; PID:g146338

GENETICS

#gene hlyA

FUNCTION

#description attacks blood cell membranes and causes cell lysis

REFERENCE S60731
#authors Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.;
Rodriguez-Barbosa, I.; Rodriguez-Ferri, E.F.
#journal Mol. Microbiol. (1994) 14:207-216
#title The RX haemolysins Apxi and Apxi2 are major virulence
factors of the swine pathogen Actinobacillus
pleuropneumoniae: evidence from mutational analysis.
#accession S60732
#status preliminary; not compared with conceptual translation
##molecule_type DNA
##residues 504-685 #label TAS
COMMENT This organism causes porcine pleuropneumonia.
GENETICS
#gene apxiA
FUNCTION
#description attacks blood cell membranes and causes cell lysis
CLASSIFICATION #superfamily hemolysin A; hemolysin A homology
#keywords calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
tandem repeat
FEATURE
243-789 #domain hemolysin A homology #label HLYA
721-847 #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYIF]-X)
721-729 #region repeat #status atypical
730-738 #region repeat #status atypical
739-747 #region repeat
748-756 #region repeat #status atypical
757-765 #region repeat
766-774 #region repeat
775-783 #region repeat
784-792 #region repeat
793-801 #region repeat
812-820 #region repeat
821-829 #region repeat #status atypical
830-838 #region repeat
839-847 #binding site palmitate (Lys) (covalent) #status
560,686 Predicted
SUMMARY
#length 1022 #molecular-weight 110013 #checksum 8625
Query Match 36.9%; Score 2291; DB 1; Length 1022;
Best Local Similarity 46.2%; Pred. No. 7,96e-295;
Matches 376; Conservative 201; Mismatches 206; Indels 31; Gaps 26;
Db 39 KQAGKLLIPKDYQAST--GSSLDLVKAAEALGIEVHRSEKNGTALAKELFGTTEKL 96
QY 11 KTGAKKLLIPYQYDTEQNGLOLVKAAEELGIEVQREERNNTAQTSLGTIQT 70
Db 97 LGFSEGIALFAPQFDKLLNKNKLSLGSSEALGQRLNKTOTALSALQSLGTIAAG 156
QY 71 IGLTERGIVLSAQIDKLLQKT-KAGALG-SAESIVQNKAKTVLSGTSILGSVLG 128
Db 157 MDLSDLLRRRNGEDVSGSELAKAGVDLAALQVDNTASATGTVDFAEAGLKGALNSNT 216
QY 129 MDLDEALQNNNS-OH---A-LAKAGLELTNSLTENIANSVKTLDFEGEQISQFGSKLNI 183
Db 217 R-LSGLASKLNLPDLISLAPGPDVAGSILSVVSASFILSNKNDADACTKAAAGIEISTKI 275
QY 184 KGLGTGDKLKNLGGDLKAGLDVIGSLGSGATLAALVLDKNAKTAKYAGFELANQV 243
Db 276 LGNIGKAVSYIIAQRVAAGLSTTAATGGTIGSVVLAISPLFLNVADRFERAKOLEQY 335
QY 244 VGNITKAVSYIIAQRVAAGLSTGPVVAIIASTVLSAISPLAFAGTADFNHAKLSLEY 303
Db 336 SERFKFEGEDSLLASFYRETGAIEAALTINSVLSSAASAGVGAATGSLVGAAPVAALV 395
QY 304 AERFKKLGVDGNLLAEYRGRTGTIDASVTAINALAAIAGSVSAAAGSVIASPIALLV 363
Db 396 SAITGIISGLIDASKAIFERVATKANKIDWEKK-HGKNYFENGVDARHSFLEDTFE 454
QY 364 SGITGVISTLIQSKQAMFHFVANKIHNKIVEKNHNGKNYFENGVDARYLANLOQNMK 423
Db 455 LLSQYNKEYSVERVAITQORWDVNGELAGITRKGSDDTKSGKAYVDFFEGKLEKEPD 514

QY 424 FLNLNKLQAEARVIAITQQOWDNNIGDLAGISRLGEKVLGKAYVDAFEKGHI-K-AD 481
Db 515 RDKKVFDPLEKIDLSSNKT-TL-LKFVTPVFAEIRERKQTKGKYEYMTLEFVKK 572
QY 482 KLVQ--LDSANGIIDVNSGKAKTHILPTPLTPGTEHREVRVOTGYEYITKLINRV 539
Db 573 EKVVVTGVOSHNAIYDTNLIQ-LAID-RK-GE--K-RQVTTIESHLGKENDRIYLSGSS 626
QY 540 DSKWITDGA--STFDLTNVVORIGIELDNAGNVTKETKIIAKLCEGDDNVFVSGIT 598
Db 627 IYVAGNGHDVAYYKTDCTGYLFDGQSAQAGEYIYVKELKADVKVLKEVKTQDISVGK 686
QY 599 EIDGGEYDRVHYSRGNYGALTIDATKETEQGSYTVRNFVETG-KALHEVTSHTALVGN 657
Db 687 RSEKLEYRYEYELSPFELNGIRAKDELHVSVEELIGSNRDKFKGSRFTDIFHGAKGDEI 746
QY 658 REEKIEYRSHN-NQHHAGY-Y-TKDTLKAVEELIGTSHNDIFKSGKFNDAFNGGVDTI 714
Db 747 YGNDGHDILYGGDNDVIVGGDNDHLVGGNDRLIGGKGN-FLN-GDGDELOVFE 804
QY 715 DNGDNDRLFGGKDDILGNGDGFIDGKGNLDLHGKGGDIFVHRKGDGNDITDSD 774
Db 805 GQYNVLGAG-NDILYSGDGTNLFDGNGVNDKI 837
QY 775 GNDKLSFSDSNLKLDFEKVKHNLVITNSKKEV 808
RESULT 11
ENTRY #type complete
TITLE leukotoxin A - Actinobacillus actinomycetemcomitans
ORGANISM #formal_name Actinobacillus actinomycetemcomitans
DATE 16-Sep-1992 #sequence_revision 01-Nov-1996 #text_change
06-Dec-1996
ACCESSIONS A37205; A60768; B34345; A32276; PH0267; PH0266; S17284
REFERENCE A37205
#authors Kraig, E.; Dailey, T.; Kolodrubetz, D.
#journal Infect. Immun. (1990) 58:920-929
#title Nucleotide sequence of the leukotoxin gene from
Actinobacillus actinomycetemcomitans: homology to the
alpha-hemolysin/leukotoxin gene family.
#cross-references MUID:90202154
#accession A37205
#molecule_type DNA
##residues 1-1055 #label KRA
##cross-references GB:X16829; PID:g38645
##note the authors present evidence that the nucleotide
sequence is correct in the vicinity of amino acid 926;
the sequence B34345 differs after this residue as a
result of a frameshift from one missing nucleotide
REFERENCE A60768
#authors Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraig, E.
#journal Infect. Immun. (1989) 57:1465-1469
#title Cloning and expression of the leukotoxin gene from
Actinobacillus actinomycetemcomitans.
#accession A60768
#status nucleic acid sequence not shown; not compared with
conceptual translation
##molecule_type DNA
##residues 297-309, 'Y', 311-364; 434-440, 'KC', 443-474, 'H', 476-489,
'S', 491-493, 'VLK', 497-498 #label KOL
##note this preliminary sequence has been revised in reference
A37205
REFERENCE A34345
#authors Lally, E.T.; Golub, E.E.; Kieba, I.R.; Taichman, N.S.;
Rosenbloom, J.; Rosenbloom, J.C.; Gibson, C.W.; Demuth,
D.R.
#journal J. Biol. Chem. (1989) 264:15451-15456
#title Analysis of the Actinobacillus actinomycetemcomitans
leukotoxin gene. Delineation of unique features and
comparison to homologous toxins.
#cross-references MUID:89359382
#accession B34345
#molecule_type DNA

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##residues      1-239,'Y',241-259,'H',261-335,'A',337-415,'S',417-438,
                  'S',440-723,'N',725-926,
                  'VHDRLNLSYSEVSTNHSIKKLSVKMGSGLLRTLIIFLIR',
                  'VGTQRQLHSLPDLRIKVSQVALCLLVROCLHKSPVQCMILVYLFQOPV
                  VLHV', 'PVKRYPLRCHRPITLTQIR' ##label LAL
##cross-references GB:M27933
REFERENCE
#authors      Lally, E.T.; Kleba, I.R.; Demuth, D.R.; Rosenbloom, J.;
#journal      Golub, E.E.; Tachman, N.S.; Gibson, C.W.
#journal      Biochem. Biophys. Res. Commun. (1989) 159:256-262
#title        Identification and expression of the Actinobacillus
                  actinomycetemcomitans leukotoxin gene.
#cross-references MUID:89165863
#accession    A32276
#status       nucleic acid sequence not shown; not compared with
                  conceptual translation
#molecule_type DNA
##residues    430-438,'S',440-476,'R',478-506,'RVRS',511,
                  'QSIASINLND',523-541,'I',543,'POV', 'RKG',556,'A',
                  558-589,'MIFY',594-689,'ST',693-723,'N',725-754
                  #label LA2
##note        this preliminary sequence has been revised in reference
                  A34345
REFERENCE      PH0266
#authors      Ohta, H.; Miyagi, A.; Kato, K.; Fukui, K.
#submission   submitted to JIPID, July 1995
#description   Modulation of leukotoxin production by growth rate and
                  bicarbonate in a toxin production-variable strain of
                  Actinobacillus actinomycetemcomitans.
#accession    PH0267
#molecule_type protein
##residues    17-42 ##label OHT
##experimental_source strain 301-b
#accession    PH0266
#molecule_type protein
##residues    2-6,'L',8-26 ##label OH2
COMMENT       This organism is implicated in juvenile periodontitis.
GENETICS
#gene         ltxA
FUNCTION
#description   lyses human polymorphonuclear lymphocytes and monocytes
CLASSIFICATION superfamily hemolysin A; hemolysin A homology
KEYWORDS       cytolysis; hemolysis; lipoprotein; periplasmic space; tandem
                  repeat
FEATURE
245-790        #domain hemolysin A homology #label HLYA\
731-847        #region 9-residue repeats (G-X-G-[DN]-D-X-[LVIYF]-X)\
741-739        #region repeat #status atypical\
740-748        #region repeat\
749-757        #region repeat\
758-766        #region repeat\
767-775        #region repeat\
776-784        #region repeat\
785-793        #region repeat #status atypical\
794-802        #region repeat\
803-811        #region repeat\
812-820        #region repeat\
821-829        #region repeat\
830-838        #region repeat\
839-847        #region repeat\
562,687        #binding_site palmitate (Lys) (covalent) #status
                  predicted
SUMMARY
#length 1055 #molecular-weight 113853 #checksum 7343
Query Match    35.5%; Score 2207; DB 1; Length 1055;
Best Local Similarity 46.1%; Pred. No. 7,59e-283;
Matches 371; Conservative 189; Mismatches 210; Indels 34; Gaps 25;
Db 44 KTG-KKLILYIPKNVK-----KNGLTALIKAAQKIGIEVYHGGKDPALTNGILNTGKGL 98
QY 11 KTGAKKILYIPONYQYDTEQNGQLDLKAAAEELGIEVQREERNIATQTSLSGTIQT 70
Db 99 LGUTERGLTFAPELDKWKIOGNKHLNSVGSTGNLTKAIDKQVSGLTGLQAFLNTAFSGM 158

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QY 71 IGLTERGVLSAPQDKLQRTKA-QGALGSAESIVQANKAKTVLSGIQSLGSLVLAGM 129
Db 159 DLDALIKARQGNKNTVDQLAKASLNLINELIGTISSTINNVDTFSKQLNKLGEALGOVK 218
QY 130 DLDEAL---QNSN-QHA-LAKAGLELNSLIENIANSVKTLDEGEQISOFGSKLQNIK 184
Db 219 HFGSPGDKLKLPLKGNLKGKLGALSGVLSAISALLANKADADATATKAAAAEUTNKVL 278
QY 185 GLGTLDGDKLKNIGGLDKAGLDVIGLLSGATAALVALADNASTAKKVGAGFELANOV 244
Db 279 GNIGKAITOYLIAORAAAGLSTTGPVAGLIAVSVLSLSPSLGIAKQFDRARMLREYS 338
QY 245 GNITKAVSSYILAQRVAAGLSTGTPVAALIASTVSLAISPFAAGIADKFNHAKSLESYA 304
Db 339 KRFKFGYNGDSLGLQFYKNTGIADAAITTTIVLSAIAAGVSAAGSLVGAPIGLLVS 398
QY 305 EREKFLGYDGNLLAEYQRTGTTDASVTAINALAAAGVSAAGSVTASPIALLVS 364
Db 399 AITSLISIGILDASQAVFEHIANQLADKIKAWE-NKYKNYFENGYDARHSAFLEDSUKL 457
QY 365 GITGVISTILQYSQAMPHERVANKIHKNKIVSEKNNHKNYFENGYDARYLANLQDNKF 424
Db 458 FNELRKRYKVTENILSITOQGWDRIGELAGITRNGDRIOQSKAYVDYLLKGEELAKHSDK 517
QY 425 LNLNKELOAQERVAITATQOQWNNIGDLGASRLGKVLGSKAYVDAFEKGKHI-K-ADK 482
Db 518 FTKQLDLPKINIDLSGI-KGSTA-LTEPLNPLTAGKERKTRQSGKYEFITEKLVKRGRT 575
QY 483 LV-Q-LDSANGIIDVNSGKAKTQHILFRTPLTPGTEHREVRVQTKVEYITKLININ-RV 539
Db 576 D-WKVGVPSNGVYDFSNLIQH-AVTRDN--KVL---EARLIANLGAKKDDYVFGSGST 628
QY 540 DSWKITDGAASS-TFDLTNVYQRIEILDNAGNVTKTKETKIIAKLGEEDDNVFGSGTT 598
Db 629 IVNAGDGYVDVYSGKRTGALTIDGRNATKAGQYKVERDLSTQVLOQTVSKQETKRKV 688
QY 599 EIDGEGGYDRVHYSNGNYGALTIDATKETEQGSYTVNRFVETGRALHEVTHHTALVGNR 658
Db 689 TDLLEYRNYKLDYVYTNKGFKAHDELNSVEITIGSTRDKFYGSKFNDFVFGHGDGDDLIY 748
QY 659 EEKIEYRHSN-NQHA--GYITKDTLKAVEILIGTSHNDIFKSGKFNDAFNGGQVDTID 715
Db 749 GYDGDRLYNGNDIETHGGGNGKLYGGAGNDRLFGYGN--YLD-GGEGDDHLEGGNG 806
QY 716 GNDGNDRLFGGKGDILDGGNGDDFDGCKGNLHGGKDDIFVHRKGGDNDIITSDSG 775
Db 807 SDILRGGSGNDK-L-FGNQGGDLL 828
QY 776 NDKLSFSDSNLKDLTTFEKVKHNLV 799
RESULT 12
ENTRY      S34238 #type fragment
TITLE      leukotoxin A - Pasteurella haemolytica (fragment)
ALTERNATE_NAMES ltxA protein
ORGANISM   #formal_name Pasteurella haemolytica
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
ACCESSIONS S34238; S34236
REFERENCE   S34235
#authors   Lalinson, A.F.; Aitchison, K.D.; Donachie, W.
#submission submitted to the EMBL Data Library, June 1993
#description DNA sequence of the carboxy terminal end of leukotoxin A from
                  the T4 serotype of Pasteurella haemolytica; DNA sequence of
                  the carboxy terminal end of leukotoxin A from the T15
                  serotype of Pasteurella haemolytica.
#accession S34238
#status     preliminary
#molecule_type DNA
##residues 1-208 ##label LA1
##cross-references EMBL:222885; PID:g311831
##experimental_source serotype T4

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#accession S34236
#status Preliminary
#molecule_type DNA
#residues 9-208 #label LA2
#cross-references EMBL:422886; PID:g311827
#experimental_source serotype T15
GENETICS
#gene lktA
CLASSIFICATION #superfamily hemolysin A; hemolysin A homology
KEYWORDS calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
          tandem repeat
SUMMARY #length 208 #checksum 8349
Query Match 19.4%; Score 1208; DB 2; Length 208;
Best Local Similarity 82.2%; Pred. No. 1.43e-141;
Matches 171; Conservative 21; Mismatches 16; Indels 0; Gaps 0;
Db 1 GNDRLFGKGGDDIDGGNGDDFDGKGNDLLHGGKGGDDIFVHRGGDNDSDITEGNDK 60
QY 719 GNDRLFGKGGDDIDGGNGDDFDGKGNDLLHGGKGGDDIFVHRGGDNDITDSDGNDK 778
Db 61 LSFSDSNLKDITFEKVNHLVITNTKQEKVTIQNWFREAEFAKTRINRYVATRDDEIEII 120
QY 779 LSFSDSNLKDITFEKVNHLVITNTKQEKVTIQNWFREAEFAKTRINRYVATRDDEIEII 838
Db 121 GNGERITSKQVDELEIKGKIDKSDLSQVVDNTQLLYKSRDASNSLDKLSSASFTS 180
QY 839 GNGERITSKQVDDLIKANGKITQDELKSVYDNYELLKHSKNVTNSLDKLSSVSFTS 898
Db 181 SNDNRNLASPTSMLDPSLSIOFARAA 208
QY 899 SNDNRNLVAPITSMLDQSLSSLOFARGS 926
RESULT 13
ENTRY #type complete
TITLE cyclolysin - Bordetella pertussis
ALTERNATE_NAMES adenylate cyclase precursor; calmodulin-sensitive adenylate
                  cyclase-hemolysin bifunctional protein
CONTAINS adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive;
          hemolysin
ORGANISM #formal_name Bordetella pertussis
DATE 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
ACCESSIONS S00893; S14100; S02389
REFERENCE Glaser, P.; Ladant, D.; Sezer, O.; Pichot, F.; Ullmann, A.;
          Danchin, A.
#journal Mol. Microbiol. (1988) 2:19-30
#title The calmodulin-sensitive adenylate cyclase of Bordetella
          pertussis: cloning and expression in Escherichia coli.
#cross-references MUID:88216178
#accession S00893
#molecule_type DNA
#residues 1-1706 #label GUA
#cross-references EMBL:Y00545; NID:g396665; PID:g396666
REFERENCE S02386
#authors Glaser, P.; Sakamoto, H.; Bellalou, J.; Ullmann, A.; Danchin,
          A.
#journal EMBO J. (1988) 7:3997-4004
#title Secretion of cyclolysin, the calmodulin-sensitive adenylate
          cyclase-haemolysin bifunctional protein of Bordetella
          pertussis.
#cross-references MUID:89091151
#contents annotation: identification of adenylate cyclase--hemolysin
          bifunctional protein
REFERENCE S14100
#authors Munier, H.; Gilles, A.M.; Glaser, P.; Krin, E.; Danchin, A.;
          Sarfati, R.; Barzu, O.
#journal Eur. J. Biochem. (1991) 196:469-474
#title Isolation and characterization of catalytic and
          calmodulin-binding domains of Bordetella pertussis
          adenylate cyclase.

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#cross-references MUID:91177021
#accession S14100
#molecule_type protein
#residues 1-78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
#label MUN
REFERENCE A55167
#authors Hackett, M.; Guo, L.; Shabanowitz, J.; Hunt, D.F.; Hewlett,
          E.L.
#journal Science (1994) 266:433-435
#title Internal lysine palmitoylation in adenylate cyclase toxin
          from Bordetella pertussis.
#contents annotation: lysine palmitoylation
          B. pertussis the etiological agent of whooping cough, disrupts
          mammalian cell function by causing elevation of cAMP
          concentration. The enhancement of cAMP synthesis is partly due to
          activation by host cell calmodulin of the adenylate cyclase
          activity of bacterial cyclolysin, which is synthesized as a large
          bifunctional precursor also carrying hemolytic activities.
          Adenylate cyclase activity is activated upon binding of calmodulin
          in the vicinity of Trp-242.
GENETICS
#gene cyaA; cya
CLASSIFICATION #superfamily cyclolysin; calmodulin-sensitive adenylate
                  cyclase catalytic domain homology; hemolysin A homology
KEYWORDS calcium binding; calmodulin binding; cAMP biosynthesis;
          carbon-oxygen lyase; hemolysis; lipoprotein;
          phosphorus-oxygen lyase; tandem repeat; toxin; whooping
          cough
FEATURE 15-328 #domain calmodulin-sensitive adenylate cyclase catalytic
                domain homology #label ADE\
                25-35 #region calmodulin binding #status predicted\
                59-66 #region nucleotide binding #status predicted\
                544-1085 #domain hemolysin A homology #label HEM\
                1033-1041,
                1042-1050,
                1174-1182,
                1289-1297,
                1298-1308,
                1316-1324,
                1430-1438,
                1556-1564
                983
                #region repeats\
                #binding_site palmitate (Lys) (covalent) #status
                experimental
SUMMARY #length 1706 #molecular-weight 177506 #checksum 6461
Query Match 14.4%; Score 896; DB 1; Length 1706;
Best Local Similarity 32.0%; Pred. No. 2.76e-98;
Matches 191; Conservative 165; Mismatches 212; Indels 29; Gaps 26;
Db 530 GGFVAGGAMALGGIAAAGVAGMSLTD-DAPAGOKAAGAAEIALQLTGGTVELASSIAL 588
QY 197 GGLDKAGLGLDVISGLSLGATAALVLADKNASTAKKVGAFELANQVGNITKAVSSV-I 255
Db 589 ALAARGVTSGLOVAGASAGAAAGALAAALSPMEIYGLVQOSHVDQDLKLAOESSATGY 648
QY 256 -LAQ-R-VAAGLSSTGPPAALIASTVSLAISPLAFAGIADKFNHAKSLSEYAEKKILGY 312
Db 649 EGDALLAOLYRDKTAAGAVAGVSAVLSTVGAASVIAAASVVGAPVAVVTSLTGALNG 708
QY 313 GDNLLAETQRTGTDISTAVTAINALAAIAGVSAAGSVIASPIALLVSGITGVIST 372
Db 709 ILRGVQQPILIEKLANDYARKI-D-ELGGP-QAYFEKNLQARHEQLANSGLRKLADLQA 765
QY 373 ILQYSQAMFHEVANKINHKEWENKNNHKNYFENGVDARY--LANQDNMKFLNLNK 430
Db 766 GWNASVTGVTTEKSALEALATIGNADNLKSVDFVDFVQGERVAGQPVV-LDVAA 824
QY 431 ELQAEVIAITQQQNDNNGIDLAGISRLGKVLSCAKYVDVAFEECKHIKADKLVDLSAN 490
Db 825 GGIDIASR-KGERPALITITPLAAPGEEORRTKTKGSEFTTVEIVGKQDWRIRDGAA 883
QY 491 GIIDVSNSGKAKTOHILFTPLTPTGTEHREVRVOTGKYEITKLNI-NRVDWSKITDGA 549

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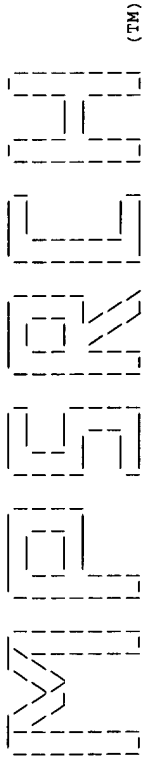
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Db 884 DTTIDLAKVVSQ-L-VD-AN-G-VLK-HSIKLDVIGGDDVVVLANSRIHYDGGAGTNTV 938
QY 550 SSTFDLNNVQRIEGLDNAGNTKTKETKIIAKLGGDDNVFVSGTTEIDGEGYDRV 609
Db 939 SYAALGRQDSITVSA--DGER--FNVRKOLNANVYREGVATQATYVKRKTENVQYRHE 994
QY 610 HYSR-GNYGALITDATKETEGGSTVYVNRFTGKALHEVSTHTALVGNREEKIEYRHSN 668
Db 994 LARVGQVVEVDTLHVQHIIIGGAGNDSITGNAHNFLLAGSGDDRLDGGAGNDTLVGGEG 1054
QY 669 NOHAGYYTKDTLKAVEREIICTSHNDIFKSKFNDAFNGGVDITDNGDNDRLFGGKG 728
Db 1055 ONTVIGGAGDDVFLDGLGVNSQLDGGAGVDTYKYNVHQPSEERLERMGDTGIHADL 1111
QY 729 DDILDGGGDD-FIDG-GKGNLHLHGKG-DDI-F-VHRKGDGN-DIITDSGNDKL 779

RESULT 14 S51672 #type complete
ENTRY cytotoxin cyclase hemolysin - Bordetella bronchiseptica
TITLE #formal_name Bordetella bronchiseptica
ORGANISM 07-May-1995 #sequence_revision 01-Sep-1995 #text_change
DATE 23-May-1997
ACCESSIONS S51672
REFERENCE S51672
#authors Betson, F.; Sismeiro, O.; Danchin, A.; Guiso, N.
#submission submitted to the EMBL Data Library, September 1994
#description The adenylate cyclase-hemolysin gene from Bordetella
bronchiseptica.
#accession S51672
#status Preliminary
#molecule_type DNA
#residues 1-1705 #label BET
##cross-references EMBL:237112
CLASSIFICATION #superfamily cyclolysin; calmodulin-sensitive adenylate
cyclase catalytic domain homology; hemolysin A homology
KEYWORDS tandem repeat
FEATURE 15-328
543-1084
SUMMARY #length 1705 #molecular-weight 177313 #checksum 3352
Query Match 14.3%; Score 887; DB 2; Length 1705;
Best Local Similarity 31.8%; Pred. No. 4.77e-97;
Matches 190; Conservative 165; Mismatches 212; Indels 30; Gaps 27;
Db 530 GGFVAGGAMALGGI-GAVGAGSLTD-DAPAGOKAAGAEIALQLTGGTVELASSTAL 587
QY 197 GLDKAGLGLDVIGLUSGATAALVLADKNASTAKKVGAGFELANQVGNITKAVSSY-I 255
Db 588 ALAARGVTSLQVAGASAGAAALAAALSPMEITYGLVQOQSHVADQLDKLAQESSAYGY 647
QY 256 -LAQ-R-VAAGLSSTGPVAAIISTVSLAISPLAFAGIADKNHAKSLESYAEERFKLGY 312
Db 648 EGDALLAOLYRDKTAEGAVAGVSAVSTVGAASVIAAASVAGPVAVTVSLTGLALNG 707
QY 313 DGDNLAAEYQRTGTIDASVTAINTALAAIAGVSAAGSVIASPIALLVSGITGVIST 372
Db 708 ILRGVQOPIIEKLANDYARKI-D-ELGGP-QAYPEKNLQARHEOLANSDDLRLKMLADLQA 764
QY 373 ILQYSKQAMFEHVANKIHNKIVWEKNNHGNKYFENGVDARY--LANIQDNKFLNLNK 430
Db 765 GWNASSVIGVQTTEISKSALEALATIGNADNLKSADEVFVDRFIQGERVAGQPVV-LDVAA 823
QY 431 ELQAEVTAITQQQWNNIGDLGISRLGEKVLGSKAVDAFEESKHKIKADKLVLQDSAN 490
Db 824 GGIDIASR-KGERPALFITPLAPGEPQRRTTKGSEFTTFVEIVGQKQDRWRIRGAA 882
QY 491 GIIDVNSGKAKTQHILFRTPLTPGTEHRRVQTKYETITKLNIRVDVSWKITDGA 549
Db 883 DTTIDLAKVVSQ-L-VD-AN-G-VLK-HSIKLEIVIGGDDVVVLANSRIHYDGGAGTNTV 937
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QY 550 SSTFDLNNVQRIEGLDNAGNTKTKETKIIAKLGGDDNVFVSGTTEIDGEGYDRV 609
Db 938 SYAALGRQDSITVSA--DGER--FNVRKOLNANVYREGVATQATYVKRKTENVQYRHE 993
QY 610 HYSR-GNYGALITDATKETEGGSTVYVNRFTGKALHEVSTHTALVGNREEKIEYRHSN 668
Db 994 LARVGQVVEVDTLHVQHIIIGGAGNDSITGNAHNFLLAGSGDDRLDGGAGNDTLVGGEG 1053
QY 669 NOHAGYYTKDTLKAVEREIICTSHNDIFKSKFNDAFNGGVDITDNGDNDRLFGGKG 728
Db 1054 HNTVVGAGDDVFLDGLGVNSQLDGGAGVDTYKYNVHQPSEERLERMGDTGIHADL 1110
QY 729 DDILDGGGDD-FIDG-GKGNLHLHGKG-DDI-F-VHRKGDGN-DIITDSGNDKL 779

RESULT 15 S35027 #type complete
ENTRY cytotoxin RTX homolog frpC - Neisseria meningitidis
TITLE #formal_name Neisseria meningitidis
ORGANISM 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
DATE 09-Sep-1997
ACCESSIONS S35027
REFERENCE S35026
#authors Thompson, S.A.; Wang, L.L.; Sparling, P.F.
#journal Mol. Microbiol. (1993) 9:85-96
#title Cloning and nucleotide sequence of frpC, a second gene from
Neisseria meningitidis encoding a protein similar to RTX
cytotoxins.
#accession S35027
#molecule_type DNA
#residues 1-1829 #label THO
##cross-references GB:L06299; NID:g293961; PID:g293963
GENETICS frpC
SUMMARY #length 1829 #molecular-weight 197622 #checksum 8960
Query Match 4.6%; Score 286; DB 2; Length 1829;
Best Local Similarity 31.8%; Pred. No. 7.59e-18;
Matches 70; Conservative 60; Mismatches 71; Indels 19; Gaps 18;
Db 952 AKDDSGOVTVQSYFONDGSGAYRTDEIHFONGKVL-DVATV-KELVQOSTDSDRLYAYQ 1009
QY 612 SRNGYGALTIDATKETE-QGSYTVNRF-VETGKALHEVSTHTALVGNREEKIE--YR-H 666
Db 1010 SGNTLNGGL-GDDYLYGADGDDLLNGDAGNDSIYSGNG-NDTLNGGEGNDALYGYNGDA 1067
QY 667 SNNQHHAGYYTKDTL-KA-VEEII-G-TSHNDFKSGKFNDAFNGGVDITDNGDNDR 722
Db 1068 LNGGEGNDHLNGEDGNDTLIGGAGNDYLEGSGSDIYVFGKFGODTVYNYDYATGRKDI 1127
QY 723 LFGGKGDDILDGGGDDFIDGKGNDLLHGKGGDIFVHRKKGNDII-T-D-SDG-NDK 778
Db 1128 IRTDGTADMLAFTTREGNHLIIKAKDGSQGVTVQSYFQN 1167
QY 779 LSFSDSNLKD-LIFERVKVHNLVI-TNSKKEKVTIQNWFE 816

Search completed: Wed Dec 9 19:23:12 1998
Job time : 176 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Dec 9 19:23:29 1998; MasPar time 25.63 Seconds
980.165 Million cell updates/sec
Tabular output not generated.

Title: >US-08-455-970-12
Description: (1-936) from US08455970.pep
Perfect Score: 6217
Sequence: 1 MATVIDLSPFKTGAKKILY.....LSSLOFARGSQHWSYGLRPG 936

Scoring table: PAM 150
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swissprot

Statistics: Mean 57.021; Variance 139.964; scale 0.407

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	6049	97.3	953	1	HLA1_PASHA	0.00e+00
2	5743	92.4	953	1	HLA3_PASHA	0.00e+00
3	5560	89.4	953	1	HLA3_PASHA	0.00e+00
4	5510	88.6	955	1	HLA3_PASHA	0.00e+00
5	5020	80.7	947	1	HLA1_PASP	0.00e+00
6	4354	68.4	956	1	RT2A_ACTPL	0.00e+00
7	4205	67.6	956	1	HLA1_ACTSU	0.00e+00
8	2616	42.1	1052	1	RT31_ACTPL	0.00e+00
9	2566	41.3	1049	1	RT31_ACTPL	0.00e+00
10	2398	38.6	1023	1	HLV1_ECOLI	0.00e+00
11	2384	38.3	1024	1	HLV1_ECOLI	0.00e+00
12	2244	36.1	1023	1	RT12_ACTPL	0.00e+00
13	2236	36.0	1023	1	RT11_ACTPL	0.00e+00
14	2167	34.9	1050	1	HLV1_ACTAC	0.00e+00
15	896	14.4	1706	1	CYAA_BORPE	9.23e-119
16	887	14.3	1705	1	CYAA_BORPE	2.89e-117
17	286	4.6	1829	1	FRPC_NEIME	8.54e-22
18	265	4.3	1115	1	FRPA_NEIME	8.30e-19
19	202	3.2	491	1	ZAPA_PROMI	3.02e-10
20	187	3.0	476	1	LIPB_PSEFL	2.52e-08
21	173	2.8	284	1	NODO_RHILV	1.38e-06
22	165	2.7	475	1	PRTG_ERWCH	1.29e-05
23	166	2.7	479	1	PRTC_ERWCH	9.75e-06

24	170	2.7	481	1	PRTB_ERWCH	SECRETED PROTEASE B PR	3.21e-06
25	164	2.6	472	1	PRTA_ERWCH	SECRETED PROTEASE A PR	1.69e-05
26	159	2.6	478	1	PRTX_ERWCH	SECRETED PROTEASE C PR	2.93e-05
27	159	2.6	3591	1	PHAB_BORPE	FILAMENTOUS HEMAGGLUTI	6.62e-05
28	152	2.4	449	1	LIPA_PSEFL	LIPASE PRECURSOR (EC 3	7.30e-04
29	150	2.4	479	1	APRA_PSEAE	ALKALINE METALLOPROTEI	4.30e-04
30	147	2.4	487	1	PRZN_SERMA	SERRALYSIN PRECURSOR (1.60e-03
31	137	2.2	1574	1	MYS2_YEAST	MYOSIN-2 ISOFORM.	2.04e-02
32	133	2.1	486	1	PRZN_SERSP	SERRALYSIN PRECURSOR (5.50e-02
33	133	2.1	550	1	KUCR_RAT	KUPFFER CELL RECEPTOR	5.50e-02
34	132	2.1	749	1	MAD1_YEAST	SPINDLE ASSEMBLY CHECK	7.02e-02
35	133	2.1	1959	1	MYSN_CHICK	MYOSIN HEAVY CHAIN, (H	5.50e-02
36	133	2.1	2035	1	HFCL_HUMAN	HOST CELL FACTOR C1 (H	5.50e-02
37	131	2.1	2249	1	190K_RICRI	190 KD ANTIGEN PRECURS	8.95e-02
38	122	2.0	390	1	FLAA_BORBR	FLAGELLIN.	7.56e-01
39	122	2.0	682	1	PILJ_PSEAE	PILJ PROTEIN.	7.56e-01
40	123	2.0	1025	1	SLAP_CAUCR	S-LAYER PROTEIN (PARAC	5.99e-01
41	124	2.0	2541	1	TALI_MOUSE	TALIN.	4.75e-01
42	121	1.9	344	1	Y09A_MYCTU	HYPOTHETICAL 35.1 KD P	9.51e-01
43	121	1.9	409	1	Y291_METJA	PROBABLE SIGNAL RECOGN	9.51e-01
44	121	1.9	754	1	KATC_ARATH	KINESIN-LIKE PROTEIN C	9.51e-01
45	121	1.9	2491	1	TALA_DICDI	FILPODIN (TALIN HOMOL	9.51e-01

ALIGNMENTS

RESULT 1	HLA1_PASHA	STANDARD;	PRT;	953 AA.
ID	PI6535;			
AC	01-AUG-1990 (REL. 15, CREATED)			
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	LEUKOTOXIN FROM SEROTYPE A1.			
GN	LKTA.			
OS	PASTURELLA HAEMOLYTICA.			
OC	PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;			
OC	PASTURELLACEAE.			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN=SEROTYPE A1;			
RX	MEDLINE: 87306837.			
RA	LO R.Y.C.; STRATHDEE C.A.; SHEWEN P.E.;			
RL	INFECT. IMMUN. 55:1987-1996(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PHL101 / SEROTYPE A1;			
RX	MEDLINE: -89210283.			
RA	HIGHLANDER S.K.; CHIDAMBARAM M., ENGLER M.J., WEINSTOCK G.M.;			
RL	DNA 8:15-28(1989).			
RN	[3]			
RP	SEQUENCE OF 884-953 FROM N.A.			
RC	STRAIN=PHL101 / SEROTYPE A1;			
RX	MEDLINE: 90236888.			
RA	HIGHLANDER S.K.; ENGLER M.J., WEINSTOCK G.M.;			
RL	J. BACTERIOL. 172:2343-2350(1990).			
CC	-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD			
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY			
CC	DEFINED.			
CC	-1- SUBCELLULAR LOCATION: SECRETED.			
CC	-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING			
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC			
CC	ACTIVITY.			
CC	-1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE			
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).			
CC	-1- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE			
CC	STRUCTURAL TOXIN).			
DR	EMBL: M20730; G150494; -			
DR	EMBL: M24197; G150513; -			
DR	PIR: S29516; S29516.			
DR	HSSP: P02392; ICTF.			
DR	PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.			
KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;			
KW	TRANSMEMBRANE.			

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FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 297 318 POTENTIAL.
FT TRANSMEM 366 390 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH (BY SIMILARITY).
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
FT CONFLICT 409 414 FERHAN -> LSTLOI (IN REF. 2).
FT CONFLICT 742 742 D -> Y (IN REF. 2).
SQ SEQUENCE 953 AA; 101996 MW; 40FB25EB CRC32;

Query Match
Best Local Similarity 97.3%; Score 6049; DB 1; Length 953;
Matches 914; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 38 KTGAKKIILYIPONYQYDTEOGNGLQDLVKAAREELGIEVQREERNNIATAQTSLSGTIQT 97
QY 11 KTGAKKIILYIPONYQYDTEOGNGLQDLVKAAREELGIEVQREERNNIATAQTSLSGTIQT 70

Db 98 IGLTERGIVLSAPQIDKLLQKTAKAGALSAESIVQNAKAKTVLSGSIQILGSLAGMD 157
QY 71 IGLTERGIVLSAPQIDKLLQKTAKAGALSAESIVQNAKAKTVLSGSIQILGSLAGMD 130

Db 158 LDEALQNNQHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGSKLQNIKGLGTIG 217
QY 131 LDEALQNNQHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGSKLQNIKGLGTIG 190

Db 218 DKLKNGIGGLDAGLDVLSGLSGATAALVLDKNAKSTAKKVGAGFELANQVGNITKA 277
QY 191 DKLKNGIGGLDAGLDVLSGLSGATAALVLDKNAKSTAKKVGAGFELANQVGNITKA 250

Db 278 VSSYILAQRVAAGLSTGPPVAALIASTVLSLAISPLAFAGIADKFNHAKLSIESVAERFKL 337
QY 251 VSSYILAQRVAAGLSTGPPVAALIASTVLSLAISPLAFAGIADKFNHAKLSIESVAERFKL 310

Db 338 GYDGDNLLEYRGTTIDASVTAINTALAAIAGGVSAAGSIVASPIALLVSGITGYI 397
QY 311 GYDGDNLLEYRGTTIDASVTAINTALAAIAGGVSAAGSIVASPIALLVSGITGYI 370

Db 398 STILOYSKOAMFEHVANKTHNKIVENKKNHKNYFENGVDARYLANLODNKFLNLNK 457
QY 371 STILOYSKOAMFEHVANKTHNKIVENKKNHKNYFENGVDARYLANLODNKFLNLNK 430

Db 458 ELQAEVIAITQQQDNNGIDLAGISRLGKVLGRAYVDAPFEGKHAKADKLVLQDLSAN 517
QY 431 ELQAEVIAITQQQDNNGIDLAGISRLGKVLGRAYVDAPFEGKHAKADKLVLQDLSAN 490

Db 518 GIIDVNSGAKTQHILFRPLTPTGTEHRVOTGKYEYITKLNINRVDSWKITDGAAS 577
QY 491 GIIDVNSGAKTQHILFRPLTPTGTEHRVOTGKYEYITKLNINRVDSWKITDGAAS 550

Db 578 STFDLTVNVRIGIEDLNAGNVTKTKETKIIAKLGGDDNVFVGSITTEIDGEGYDRVH 637
QY 551 STFDLTVNVRIGIEDLNAGNVTKTKETKIIAKLGGDDNVFVGSITTEIDGEGYDRVH 610

Db 638 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVNREKTEYRHSNQ 697
QY 611 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSHTALVNREKTEYRHSNQ 670

Db 698 HHAGYTTKTLKAVEEIIIGTSHNDIFKSGKFNDAFNGGQVDTIDGNDGNDRLFQGGKDD 757
QY 671 HHAGYTTKTLKAVEEIIIGTSHNDIFKSGKFNDAFNGGQVDTIDGNDGNDRLFQGGKDD 730

Db 758 ILDGGNGDDFIDGGKNDLHGGKGDIFVHRKGDNDIITSDGNDKLSFSDSNLKDIT 817
QY 731 ILDGGNGDDFIDGGKNDLHGGKGDIFVHRKGDNDIITSDGNDKLSFSDSNLKDIT 790

Db 818 FEKVKNLVTITSSKKEKVITQNWREADFAKEVPNYKATKDEKIEIIGONGERITSKOV 877
QY 791 FEKVKNLVTITSSKKEKVITQNWREADFAKEVPNYKATKDEKIEIIGONGERITSKOV 850
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Db 878 DDLIAKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISVSFAFTSSNDSRNVLVAPT 937
QY 851 DDLIAKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISVSFAFTSSNDSRNVLVAPT 910

Db 938 SMLDOSLSLQFARAA 953
QY 911 SMLDOSLSLQFARGS 926

RESULT 2
ID HLAB PASHA STANDARD; PRT; 953 AA.
AC P55118;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN FROM SEROTYPE A11.
GN LKTA.
OS PASTEURILLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE A11;
RX MEDLINE; 94041617.
RA BURROWS L.L., OLAH-WINFIELD E., LO R.Y.C.;
RL INFECT. IMMUN. 61:5001-5007(1993).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN).
DR EMBL; U01215; G397992; -.
KW PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 230 250 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH.
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
SQ SEQUENCE 953 AA; 102206 MW; 321C9369 CRC32;

Query Match
Best Local Similarity 92.4%; Score 5743; DB 1; Length 953;
Matches 856; Conservative 37; Mismatches 23; Indels 0; Gaps 0;

Db 38 KTGAKKIILYIPKDYQYDEKNGVGLQDLVKAAREELGIEVQREERNNIATAQTSLSGTIQT 97
QY 11 KTGAKKIILYIPQYDTEOGNGLQDLVKAAREELGIEVQREERNNIATAQTSLSGTIQT 70

Db 98 IGLTERGIVLSAPQIDKLLQKTAKAGALSAESIVQNAKAKTVLSGSIQILGSLAGMD 157
QY 71 IGLTERGIVLSAPQIDKLLQKTAKAGALSAESIVQNAKAKTVLSGSIQILGSLAGMD 130

Db 158 LDEALQNNQHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGSKLQNIKGLGTIG 217
QY 131 LDEALQNNQHALAKAGLELTNSLIENIANSVKTLDGFGQISQFSGSKLQNIKGLGTIG 190

Db 218 DKLKGLSGFDKTSGLDGVVSGLLSGATAALVLDKNAKSTAKKVGAGFELANQVGNITKA 277
QY 191 DKLKNGIGGLDAGLDVLSGLSGATAALVLDKNAKSTAKKVGAGFELANQVGNITKA 250
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Db 278 VSSYLAORVAAGLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 337
Qy 251 VSSYLAORVAAGLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 310
Db 338 GYDGNLLAEYQRTGTTIDRSVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 397
Qy 311 GYDGNLLAEYQRTGTTIDRSVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 370
Db 398 STILOYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGVDARYLANLODNMKFLNLNK 457
Qy 371 STILOYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGVDARYLANLODNMKFLNLNK 430
Db 458 ELQAEVTAITQQQNDNIGDLGSRGKVLGSKAYDAFEKGKHLKADKLVDLSAN 517
Qy 431 ELQAEVTAITQQQNDNIGDLGSRGKVLGSKAYDAFEKGKHLKADKLVDLSAN 490
Db 518 GIIDVSNKSKAKTOHILFRTPLTPGTEHRRVOTGKYEYITKLNINRVDSWKIIDGAAS 577
Qy 491 GIIDVSNKSKAKTOHILFRTPLTPGTEHRRVOTGKYEYITKLNINRVDSWKIIDGAAS 550
Db 578 STFDLTNNVQRIEIDNAGNVTKTKETKIIAKLGEGDDNVFVSGTTEIDGEGYDRVH 637
Qy 551 STFDLTNNVQRIEIDNAGNVTKTKETKIIAKLGEGDDNVFVSGTTEIDGEGYDRVH 610
Db 638 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 697
Qy 611 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 670
Db 698 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNKNDRLFGKGGD 757
Qy 671 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNKNDRLFGKGGD 730
Db 758 IIDGNGDDFIDGKGNLHGGKGGDIFVHRQDGNDIITSDGNDKLSFSDSNLKDIT 817
Qy 731 IIDGNGDDFIDGKGNLHGGKGGDIFVHRQDGNDIITSDGNDKLSFSDSNLKDIT 790
Db 818 FEKVHNLVITNSKEKVTIQDFREDAFKEVRYNKKATKDEKIEIIGQNGERITSQV 877
Qy 791 FEKVHNLVITNSKEKVTIQDFREDAFKEVRYNKKATKDEKIEIIGQNGERITSQV 850
Db 878 DDLIAGKNGKITQDELKSKVDNYELLKSKNVTNSLDKLISASAFSTNSDRNVLVAPT 937
Qy 851 DDLIAGKNGKITQDELKSKVDNYELLKSKNVTNSLDKLISASAFSTNSDRNVLVAPT 910
Db 938 SMDQSLSSLOFARAA 953
Qy 911 SMDQSLSSLOFARAGS 926

RESULT 3
ID HLA3-PASHA STANDARD: PRT: 953 AA.
AC P55116;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN FROM SEROTYPE T3.
GN LKTA.
OS PASTEURCELLA HAEMOLYTICA.
OC PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURCELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE T3;
RX MEDLINE; 94041617.
RA BURROWS L.L., LO R.Y., OLAH-WINFELD E.;
RL INFECT. IMMUN. 61:5001-5007(1993).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC -!- CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC

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CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL; U01216; G397995; -.
KW PROSITE; PS00330; HEMOLYSIN-CALCIUM; 2.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 297 318 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
FT DOMAIN 734 784 6 X REPEATS, GLY-RICH.
FT REPEAT 734 739 1.
FT REPEAT 743 748 2.
FT REPEAT 752 757 3.
FT REPEAT 761 766 4.
FT REPEAT 770 775 5.
FT REPEAT 779 784 6.
SQ SEQUENCE 953 AA; 101948 MW; FFED778E CRC32;

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Query Match 89.4%; Score 5560; DB 1; Length 953;
Best Local Similarity 89.2%; Pred. No. 0.00e+00;
Matches 817; Conservative 55; Mismatches 44; Indels 0; Gaps 0;

Db 38 KNGVKKIILYIPKDYKSDSGNGLDLVKAAEELGIEVQKEEGNDIAKAQTSIGTQNV 97
Qy 11 KTGAKKIILYIPQNYQYDEQNGLDLVKAAEELGIEVQKEEGNDIAKAQTSIGTQ 70
Db 98 LGLTERGVLSAPOLDKLLQNKVQALGSSSEIAQNFQAKTVLGSVQSILGSLVAGMD 157
Qy 71 LGLTERGVLSAPOLDKLLQNKVQALGSSSEIAQNFQAKTVLGSVQSILGSLVAGMD 130
Db 158 LDEALQNESDQTLAKAGLELTNSLIENANSVOTLDAFSEQISQFQKLNQVKGALG 217
Qy 131 LDEALQNNQNHAKAGLELTNSLIENANSVOTLDAFSEQISQFQKLNQVKGALG 190
Db 218 DKLKNIGGLDAGLGLHVISGLSGATAALVADKADSTAKKVGAGFELANOVGNITKA 277
Qy 191 DKLKNIGGLDAGLGLHVISGLSGATAALVADKADSTAKKVGAGFELANOVGNITKA 250
Db 278 VSSYLAORVAARLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 337
Qy 251 VSSYLAORVAARLSSTGPVAALIASTVSLAISPAGIADKFNHAKSLESYAERFKL 310
Db 338 GYEGDLSLAIEYQHGTTIDASVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 397
Qy 311 GYEGDLSLAIEYQHGTTIDASVTAINTALAAIAGVSAAGRSVIASPIALVSGITGVI 370
Db 398 STILOYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGVDARYLANLODNMKFLNLNK 457
Qy 371 STILOYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGVDARYLANLODNMKFLNLNK 430
Db 458 ELQAEVTAITQQQNDNIGDLGSRGKVLGSKAYDAFEKGKHLKADKLVDLSAN 517
Qy 431 ELQAEVTAITQQQNDNIGDLGSRGKVLGSKAYDAFEKGKHLKADKLVDLSAN 490
Db 518 GIIDVSNKSKAKTOHILFRTPLTPGTEHRRVOTGKYEYITKLNINRVDSWKIIDGAAS 577
Qy 491 GIIDVSNKSKAKTOHILFRTPLTPGTEHRRVOTGKYEYITKLNINRVDSWKIIDGAAS 550
Db 578 STFDLTNNVQRIEIDNAGNVTKTKETKIIAKLGEGDDNVFVSGTTEIDGEGYDRVH 637
Qy 551 STFDLTNNVQRIEIDNAGNVTKTKETKIIAKLGEGDDNVFVSGTTEIDGEGYDRVH 610
Db 638 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 697
Qy 611 YSRGNYGALTIDATKETEKGSTVNRVETGKALHEGTSHTALVGNREEKIEYRHSNNQ 670
Db 698 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNKNDRLFGKGGD 757
Qy 671 HHAGYTTKDTLKAEEIIGTSHNDIFKSKFNDAFNGGVDITDGNKNDRLFGKGGD 730

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Db 758 IIDGGNGDDFDGKGNHLLHGGKGVDFVHROGDGNDSTITESGNDKLSFSDSNLKDLT 817
 Qy 731 ILDDGGNGDDFDGKGNHLLHGGKGVDFVHROGDGNDSTITESGNDKLSFSDSNLKDLT 790
 Db 818 FEKVNHLVITNTKQEVKTQNWFRFAEFAKTQNYVATRDCKIEEIIQNGERITSKVQV 877
 Qy 791 FEKVKHNLVITNSKKEVKTQNWFRFAEFAKTQNYVATRDCKIEEIIQNGERITSKVQV 850
 Db 878 DDLIAGKNGKIAQSELTKVVDNYQLLYKSRDASNSLDKLISSAFTSSNDSRNVLASPT 937
 Qy 851 DDLIAGKNGKIQSELTKVVDNYQLLYKSRDASNSLDKLISSAFTSSNDSRNVLASPT 910
 Db 938 SMLDPSLSSIQFARAA 953
 Qy 911 SMLDQSLSSIQFARGS 926
 RESULT 4
 ID HLAAPASHA STANDARD; PRT; 955 AA.
 AC P5517; 1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE LEUKOTOXIN FROM SEROTYPE T10.
 GN LKTA.
 OS PASTURELLA HAEMOLYTICA.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC PASTURELLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC LAINSON A.F., MURRAY J., DAVIES R.C., DONACHIE W.;
 RA MICROBIOLOGY 142:2499-2507(1996).
 RL CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 CC DEFINED.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
 CC ACTIVITY.
 CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
 CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
 CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
 CC STRUCTURAL TOXIN).
 DR EMBL; 226247; G400425; -
 DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
 KW HEMOLYSIN; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 299 319 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 383 403 POTENTIAL.
 FT DOMAIN 736 786 6 X REPEATS, GLY-RICH.
 FT REPEAT 736 741 1.
 FT REPEAT 745 750 2.
 FT REPEAT 754 759 3.
 FT REPEAT 763 768 4.
 FT REPEAT 772 777 5.
 FT REPEAT 781 786 6.
 SQ SEQUENCE 955 AA; 102187 MW; AA440A0A CRC32;
 Query Match 88.6%; Score 5510; DB 1; Length 955;
 .Best Local Similarity 88.4%; Pred.No. 0.00e+00;
 Matches 810; Conservative 60; Mismatches 46; Indels 0; Gaps 0;
 Db 40 KNGAKKIILYIPKDYKDYSGSGNGQLDLVKAABELGIEVQKEEGNDIAKAQTSIGTIQNV 99
 Qy 11 KTGAKKIILYIPQYQYDTEOGNGQLDLVKAABELGIEVQKEERNNTAQTSLGTQTA 70
 Db 100 LGLTERGIVLSAPOLDKLLQNKVQALGSGSESTAQNFQSVLGVQGNRRTVLGMD 159
 Qy 71 IGLTERGIVLSAPOLDKLLQNKVQALGSGSESTAQNFQSVLGVQGNRRTVLGMD 130
 Db 160 LDEALQNESDQTLAKAGLELTNSLIENIANSVQTLDAFSEIQSGFKLQNVKGLGALG 219

Qy 131 LDERALQNSNQHALAKAGLELTNSLIENIANSVQTLDAFSEIQSGFKLQNVKGLGALG 190
 Db 220 DKLNIGGLDKAGLGLDYKSRLLSGATAALVLADKADASTAKKYAGAGFELANQVVGNTIKA 279
 Qy 191 DKLNIGGLDKAGLGLDYKSRLLSGATAALVLADKADASTAKKYAGAGFELANQVVGNTIKA 250
 Db 280 VSSYILAQRAAGLSSTGPPVAALIASTVAIVASPLSFAGIADKDFRAKSLNVAERFKKL 339
 Qy 251 VSSYILAQRAAGLSSTGPPVAALIASTVAIVASPLSFAGIADKDFRAKSLNVAERFKKL 310
 Db 340 GYEGDSLLAEVQCHGTGTDASVTAINALAAIAGGVSAAGVAVASPIALLVSGITGVI 399
 Qy 311 GYEGDSLLAEVQCHGTGTDASVTAINALAAIAGGVSAAGVAVASPIALLVSGITGVI 370
 Db 400 STILQYSQAMFEHVANKIHNKIVENKNGKYNFYNGYDARYLANLQDNMKFLLNLK 459
 Qy 371 STILQYSQAMFEHVANKIHNKIVENKNGKYNFYNGYDARYLANLQDNMKFLLNLK 430
 Db 460 ELQAEVIAITQOQWDSNIGDLAGISRLGKVLSGKAYVDAFEEGQHLKADKLVQLDSAK 519
 Qy 431 ELQAEVIAITQOQWDSNIGDLAGISRLGKVLSGKAYVDAFEEGQHLKADKLVQLDSAN 490
 Db 520 GIIDVTNTGEAKTQHILFRPLTPGTEKREYVITKLHINRVDSQIKDCAAS 579
 Qy 491 GIIDVTNTGEAKTQHILFRPLTPGTEKREYVITKLHINRVDSQIKDCAAS 550
 Db 580 STFDLTNVVQIRIGVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDGEGYDRVH 639
 Qy 551 STFDLTNVVQIRIGVELDHAENVIKTKETKIVATLGDGDDNVFVSGTTEIDGEGYDRVH 610
 Db 640 YSRNGYALTDATKETEQQSYTVNRFVSGKALHEGTSTHTALVGNREKIEYRHNNQ 699
 Qy 611 YSRNGYALTDATKETEQQSYTVNRFVSGKALHEGTSTHTALVGNREKIEYRHNNQ 670
 Db 700 HHAGYITKDTLKAEEIIGTSHNDIPKGSKFNDAGNGDGVDTIDGNDGNDRLFGGKDD 759
 Qy 671 HHAGYITKDTLKAEEIIGTSHNDIPKGSKFNDAGNGDGVDTIDGNDGNDRLFGGKDD 730
 Db 760 IIDGGNGDDFDGKGNHLLHGGKGVDFVHROGDGNDSTITESGNDKLSFSDSNLKDLT 819
 Qy 731 ILDDGGNGDDFDGKGNHLLHGGKGVDFVHROGDGNDSTITESGNDKLSFSDSNLKDLT 790
 Db 820 FEKVNHLVITNTKQEVKTQNWFRFAEFAKTQNYVATRDCKIEEIIQNGERITSKVQV 879
 Qy 791 FEKVKHNLVITNSKKEVKTQNWFRFAEFAKTQNYVATRDCKIEEIIQNGERITSKVQV 850
 Db 880 DELEKNGKIAQSELTKVVDNYQLLYKSRDASNSLDKLISSAFTSSNDSRNVLASPT 939
 Qy 851 DDLIAGKNGKIQSELTKVVDNYQLLYKSRDASNSLDKLISSAFTSSNDSRNVLASPT 910
 RESULT 5
 ID HLYA_PASSP STANDARD; PRT; 947 AA.
 AC P55123;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE LEUKOTOXIN.
 GN LKTA.
 OS PASTURELLA HAEMOLYTICA-LIKE SP. (STRAIN 5943B).
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC PASTURELLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 9329320.
 RA CHANG Y.-F., MA D.-P., SHI J., CHENGAPPA M.M.;
 RL INFECT. IMMUN. 61:2089-2095(1993).
 CC -!- FUNCTION: VIRULENCE FACTOR WHICH IS CYTOTOXIC FOR LEUKOCYTES BUT

CC IS NOT HEMOLYTIC.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
CC EMBL: L12148; G457618; ...
CC DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
CC KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
CC TRANSMEMBRANE.
FT TRANSMEM 154 170 POTENTIAL.
FT TRANSMEM 312 333 POTENTIAL.
FT TRANSMEM 393 414 POTENTIAL.
FT DOMAIN 625 780 7 X REPEATS, GLY-RICH.
FT REPEAT 625 630 1.
FT REPEAT 730 735 2.
FT REPEAT 739 744 3.
FT REPEAT 748 753 4.
FT REPEAT 757 762 5.
FT REPEAT 766 771 6.
FT REPEAT 775 780 7.
SQ SEQUENCE 947 AA; 101559 MW; 1D59473B CRC32;

Query Match 80.7%; Score 5020; DB 1; Length 947;
Best Local Similarity 78.6%; Pred. No. 0.00e+00;
Matches 720; Conservatives 121; Mismatches 73; Indels 2; Gaps 2;

Db 34 KAGAKKILYIPKDYEDVGRGQDLVKAEDLGIQVQERNGTAONSLSTIQNI 93
Y 11 KTGAKKILYIPQNYQYDEGNGLDLVKAABELGIEVQERNGTAONSLSTIQTA 70
Db 94 LGSERGVLSAPQDKLLQKYISKAPGSGSENVAKNIGNAQTLLSGIQSLGVMAGMD 153
Y 71 IGLTERGIVLSAPQIDKLLQTKAQAGLSAESIVQANAKAKTVLSGIQSLGVLGMD 130
Db 154 LDEILKNGSELDLAKAGLELTNSLIENIANSVQTLDTFSEIQSLGKLNQVGLGTG 213
Y 131 LDEALQNNSHALAKAGLELTNSLIENIANSVKTLDFEGQISQFGSKLNKGLGTG 190
Db 214 DKLNFSGFSGAGLGLVVISGLSGATAALVLADKNASTDRKVGAGFLANQVGNITKA 273
Y 191 DKLNIGGLDRAGLGLDVISGLSGATAALVLADKNASTAKRVGAGFLANQVGNITKA 250
Db 274 VSSYLAQVRAAGLSNTPGVSALIASTVALAISPLAFAGIADKFNNAKALSYAERFKL 333
Y 251 VSSYLAQVRAAGLSNTPGVAALIASTVSLAISPLAFAGIADKFNNAKALSYAERFKL 310
Db 334 GYEGDLSLAEYQRTGTDASVTAVNTALAAISGVSAAGSLVGPAILLVSGITGII 393
Y 311 GYDGNLLAEYQRTGTDASVTAVNTALAAISGVSAAGSLVGPAILLVSGITGVI 370
Db 394 STILQYSQAMFEHVANKIHDKVDEKKNHKNYFENGYSRVLADLQNNROLQNLK 453
Y 371 STILQYSQAMFEHVANKIHKNVWEKKNHKNYFENGYSRVLADLQNNKFLNLK 430
Db 454 ELQAEVIRITQQQDNNIGNLAGISRLGKVMGSKAYADAFEEGKLTAKDTFVQLDSAT 513
Y 431 ELQAEVIRITQQQDNNIGNLAGISRLGKVMGSKAYADAFEEGKLTAKDTFVQLDSAN 490
Db 514 GVINTSKDNVKTQHILFRTPLTPGVNRRIRIQTKYVEYITKLNINRVDSSWKITDGA 573
Y 491 GVIDVNSGSKAKTQHILFRTPLTPGVNRRIRIQTKYVEYITKLNINRVDSSWKITDGAAS 550
Db 574 STFDLTNNVQVQIGELHDADNVTKEKTIANLGDGNDVDFIGSGTEVDGNGLDVH 633
Y 551 STFDLTNNVQVQIGELHDADNVTKEKTIANLGDGNDVDFIGSGTEVDGNGLDVH 610
Db 634 YSRGDYALTIDATNESVQGSYTKRVFETGKALHEVATQSVLVGSREKIEYRHSNNT 693
Y 611 YSRGNYGALTIDATKETEGQSYTNVRFETGKALHEVATQSVLVGSREKIEYRHSNNO 670

Db 694 OHAGYTTDTLKSVEELIGTSRNDIFKSGFDFAFGCGVDNIDGNAGNDRFLFGGKGF 753
Y 671 HHAGYTTDTLKSVEELIGTSRNDIFKSGFDFAFGCGVDNIDGNAGNDRFLFGGKGD 730
Db 754 IIDGGDDDFIDGGQDDILHGGKNDILCTVKG-GNDSISDSGGNDRLSFADSNLKDLT 812
Y 731 ILDGGNGDDFIDGGKNDLHGGKDDIFVHRKGDGNDITDSDGNDKLSFSDSNLKDLT 790
Db 813 FEKVNHLMTNKKVKTIONMFRADYAKTVHNTQATADEKIEEIIIGRGERITSKQI 872
Y 791 FEKVKNLVITNSKKKVTIONMFRADFAKEVPNYKATKDEKIEEIIIGRGERITSQV 850
Db 873 DELIEKKGKIDQSELERIAESSALLKESKFASNLKLYSSAGAFASSNDRVGLGPT 932
Y 851 DDLIAGNGKITODELSKYVDNYELLKHKSNVTNSLKLSSVSAFTSSNDRNVLPAPT 910
Db 933 SLYEHT-QSVQFVRAA 947
Y 911 SMLDOSLSLQFARG 926

RESULT 6
ID RT2A_ACTPL STANDARD; PRT; 956 AA.
AC P15377;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DE RTX-II TOXIN DETERMINANT A (APX-IIA) (HEMOLYSIN IIA) (HLY-IIA)
DE (CYTOLYSIN IIA) (CLY-IIA).
GN APXIIA OR CIVIIA OR HLYIIA OR APPA OR CYTC.
OS ACTINOBACILLUS PLEUROPEUMONIAE (HAEMOPHILUS PLEUROPEUMONIAE).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROTYPE 5;
RX MEDLINE; 90126233.
RA CHANG Y.-F., YOUNG R., STRUCK D.K.;
RL DNA 8:635-647(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
RX MEDLINE; 92040145.
RA SMITS M.A., BRIARE J., JANSEN R., SMITH H.E., KAMP E.M.,
RA GIELKENS A.L.;
RL INFECT. IMMUN. 59:4497-4504(1991).
CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A PLEUROPEUMONIAE.
CC WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND IS MODERATELY CYTOTOXIC
CC FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
CC EMBL: M30602; G141825; -.
DR EMBL; X61111; G38941; -.
DR PIR; B33389; B33389.
DR PIR; S18853; S18853.
DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 1.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 233 256 POTENTIAL.
FT TRANSMEM 266 323 POTENTIAL.
FT TRANSMEM 361 406 POTENTIAL.
FT DOMAIN 719 787 8 X REPEATS, GLY-RICH.
FT REPEAT 719 724 1.
FT REPEAT 728 733 2.
FT REPEAT 737 742 3.
FT REPEAT 746 751 4.

[illegible]

364	QY	SGITGVISTILQYSKQAMPEHVANKTHNKIVWEKNNHGKNFYFENGYDARYLANLQDNMK	423
458	Db	ILSQYNKEYSVERSVLITOOHMDTLIGELAGVTRNGDKTLSGKSYIDYYEEGKRLKKPD	517
424	QY	FLNLNKLQEAERVAITQQQDNNGIDLAGIRGEKVLGSKAYVDAAEESGKHI--KAD	481
518	Db	EFOQVDFPLKGNIDLSDS--KSTL-LKFVTPLLTPEEIRERRRQSGKYEYITELLVKG	575
482	QY	KLV-QL-DSANGIIDVSNQKAKTOHILFRTPLTPTGTEHREVRQTKYEYITKLNIRV	539
576	Db	DKVTYGVQDKGSVDYDYNLIQHASV-----GN-NOYREIRIESHIGDGDVKVFLSAGSA	629
540	QY	DSWKITDGA--SSTFDLTNVVORIGIELDNAGNVTKETKIIAKLGEQDNVFGSGTT	598
630	Db	NIYAGKHDDVVYDKTDTGLATIDGPKATEAGNYTVRYLGGDVKVLQEVVKEQEVSVCK	689
599	QY	EIDGGEGYDRKHVYSRNGYGALTIDATKEQSGSYTVNRVETG-KALHEVITSTHTALVN	657
690	Db	RTEKTOYRSEFFTHNGKMLTETDNLISVEELTGTTTRADKFFGSKPADIFHGADGDHIE	749
658	QY	REEKIEYRHSNNQHAG-YTT-KDTLKAVEEIIGTSHNDIFRGSKEFNDAFGDGVDTID	715
750	Db	GNQDNRLYDKGNDPLSGSGDDQLYGGDNDKLGAGNN-YLN-GGDGDD	800
716	QY	GNQDNRLFGKGDDILDGGGDDFIDGGKNDLLHGGKGGDIFVHRHKGDDND	768
RESULT 11			
ID	HLYA_ECOLI	STANDARD;	PRT; 1024 AA.
AC	P08715;		
DT	01-JAN-1988 (REL. 06, CREATED)		
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)		
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)		
DE	HEMOLYSIN, PLASMID.		
GN	HLYA.		
OS	ESCHERICHIA COLI.		
OG	PLASMID PHLY152.		
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS		
OC	ENTEROBACTERIACEAE.		
RC	[1]		
RP	SEQUENCE FROM N.A.		
RL	HESS J., WELLS W., VOGEL M., GOEBEL W.;		
RL	FEMS MICROBIOL. LETT. 34:1-11(1986).		
CC	-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD		
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY		
CC	DEFINED.		
CC	-1- SUBCELLULAR LOCATION: SECRETED.		
CC	-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BENDING		
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC		
CC	ACTIVITY.		
CC	-1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE		
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.		
CC	-1- DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY BY		
CC	STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE OF THE		
CC	URINARY TRACT.		
CC	-1- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE		
CC	STRUCTURAL TOXIN).		
DR	EMBL; M14107; G150682; -		
DR	PROSITE; P500330; HEMOLYSIN_CALCIUM; 4.		
KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;		
KW	TRANSMEMBRANE; PLASMID.		
FT	TRANSMEM 238 260	POTENTIAL.	
FT	TRANSMEM 268 327	POTENTIAL.	
FT	TRANSMEM 365 411	POTENTIAL.	
FT	DOMAIN 724 870	POTENTIAL.	
FT	REPEAT 724 729	16 X REPEATS, GLY-RICH.	
FT	REPEAT 733 738	1.	
FT	REPEAT 733 738	2.	
FT	REPEAT 742 747	3.	
FT	REPEAT 751 756	4.	
FT	REPEAT 760 765	5.	
FT	REPEAT 769 774	6.	
FT	REPEAT 778 783	7.	

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FT REPEAT 787 792 8.
FT REPEAT 796 801 9.
FT REPEAT 807 812 10.
FT REPEAT 817 822 11.
FT REPEAT 826 831 12.
FT REPEAT 835 840 13.
FT REPEAT 844 849 14.
FT REPEAT 856 861 15.
FT REPEAT 865 870 16.
SQ SEQUENCE 1024 AA; 110201 MW; 38CE3D51 CRC32;

Query Match
Best Local Similarity 48.6%; Score 2384; DB 1; Length 1024;
Matches 376; Conservative 187; Mismatches 181; Indels 29; Gaps 22;

Db 43 RNAGNRLLIIPKDYK-G--QGSSNDLVRTADELGIEVQYDEKNGTALTITKQVFGTAERKL 99
QY 11 KTGAKKIILYIPQNYQDYDEQNGLDLVKAAEELGIEVQREERNIATQSLGTQTA 70
Db 100 IGLTERGVTFAPQDKLLQKYKAGNIGLGGAGNIGDNLGRAGGILSTFQNFGLTALSS 159
QY 71 IGLTERGVLSAPQDKLLQK-TRGAQLGS-AESIVQANKAKTVLSGIQISILGSVLG 128
Db 160 MKIDELIKKQSGNVSSELAKASTELINQLDVTVASLNNVNSFSOOLNTLGSVLSNT 219
QY 129 MDLDEAL--ONNS-N-OHA-LAKAGLELTNSLIENIANSVKLTDFGEOISFGSKLQNI 183
Db 220 KHLNGVGNKQLNDLNTAGLDVTSGILSAISAFILSNADADTRTKAAAGVBLTKV 279
QY 184 KGLTGLDKLKNIGLDKAGLGVISGLSGATAALVLADKNNAKTKVAGGAFELANQV 243
Db 280 LQNVKGISQYIIAQAAGGLSTSAAGLIASAVTLAISPLSFLSIADKFRANKIESEY 339
QY 244 VGNITKAVSSYIIAQAAGGLSTGPVAAIASTVSLAISPLAFAGIADKFNHAKSLESY 303
Db 340 SREFKGLGVDGSLAAPHKGTGADASTTITVLAHSVSSGISAAATSLVGPVSAIV 399
QY 304 AERFKLGVGGNGLAEYQGTGTDIDASTVNTALAAJAGVSAAGVSIAPIALLV 363
Db 400 GAVTGIISGILEAKQAMPEHVASKMADYIAEWKK-HGKNYFENGYDARHAAPLEDNFK 458
QY 364 SGITGVISTILQYSKOAMPEHVANKIHNVEMKNGHKNYFENGYDARYLANLQDNMK 423
Db 459 ILSQNKYSVRSVLITQOHHDTLIGELAGVTRNGDKTLGSKSIDYIEEGRLEKXKD 518
QY 424 FLNLNKLQAEVIAITQQQDNNIGDLGSLGKVLGSKAYVDAAFEKGHI--RAD 481
Db 519 EFQKQVDFPLKGNIDLS-KSSTL-LKFTVPLLTGPEIRERROSGKYETITELLVGV 576
QY 482 KLV-QL-DSANGIIDVNSGKAKTOHILFRLTPTGTEHREVOTGKYETITKLNIRV 539
Db 577 DKWTVGVODKGVADYDYNLIQHASV-----GN-NQYREIRIESHLGDDGDDKVFLSAGSA 630
QY 540 DSKMITDGAA-SSTFDLTNVVQIGELDNAGNVKTKETKIIAKLGEDDNNVFGSGTT 598
Db 631 NIYAKGHDVYVDKTDGTYLIDGTAKTEAGNYTVTRVLGDDGVKQVLEVEKVEQSVGK 690
QY 599 EIDGEGYDRVYSRNGYALATIDATKETEQGSYTVNREVETG-KALHEVISTHTALVGN 657
Db 691 RTEKTQYRSYETHINGKNLTETDNLVSVLEELIGTTRADKPFSGKFTDIFHCADGDDLE 750
QY 658 REEKEYHRNSNOHAG-YYT-KDTLKAAVEELIIGTSHNDIFKGSFNAFNGGDDGVDITD 715
Db 751 GNDGNDRLYDGNNDTLGSGNGDDQLYGDDGNDKLGIVAGNN-YLN-GGDGDD 801
QY 716 GNDGNDRLFGGKDDLLDGGNGDDFIDGGKGNDDLHGKGGDDIFVHRKGDGND 768

RESULT 12
ID RT12.ACTPL STANDARD; PRT: 1023 AA.
AC P55129;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

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DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE RTX-1 TOXIN DETERMINANT A FROM SEROTYPES 5/10 (APX-1A) (HEMOLYSIN 1A)
DE (HLY-1A) (CYTOLYSIN 1A) (CLY-1A).
GN APXIA OR CLYIA OR HLYIA.
OS ACTINOBACILLUS PLEUROPNEUMONIAE (HAEMOPHILUS PLEUROPNEUMONIAE).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-13039 / SEROTYPE 10;
RX MEDLINE: 94276858.
RA NAGAI S., YAGIHASHI T., ISHIHAMA A.;
RL MICROB. PATHOG. 15:485-495(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K17 / SEROTYPE 5;
RX MEDLINE: 96401417.
RA CHIN N., FREY J., CHANG C.F., CHANG Y.F.;
RL FEMS MICROBIOL. LETT. 143:1-6(1996).
RN [3]
RP SEQUENCE OF 886-1023 FROM N.A.
RC STRAIN-K17 / SEROTYPE 5;
RX MEDLINE: 93366425.
RA JANSEN R., BRIAIRE J., KAMP E.M., GIELKENS A.L.J., SMITS M.A.;
RL INFECT. IMMUN. 61:3688-3695(1993).
CC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
CC WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
CC ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -1- APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7, 8, 12, AND
CC TOTALLY DELETED IN SEROTYPE 3.
CC -1- THE SEQUENCE SHOWN IS THAT OF SEROTYPE 10.
CC -1- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL: D16582; G497787; -.
DR EMBL: U04954; G1477457; -.
DR EMBL: X73116; G312215; -.
DR PROSITE: PS00330; HEMOLYSIN_CALCIUM; 2.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 226 256 POTENTIAL.
FT TRANSMEM 297 326 POTENTIAL.
FT TRANSMEM 367 406 POTENTIAL.
FT DOMAIN 722 845 13 X REPEATS, GLY-RICH.
FT REPEAT 722 727 1.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 813 818 10.
FT REPEAT 822 827 11.
FT REPEAT 831 836 12.
FT REPEAT 840 845 13.
FT CONFLICT 210 217 AMPYLTLA -> GNALSNT (IN REF. 2).
FT CONFLICT 581 581 E -> Q (IN REF. 2).
FT CONFLICT 687 688 TC -> R (IN REF. 2).
FT CONFLICT 1015 1015 F -> L (IN REF. 2).
SQ SEQUENCE 1023 AA; 110129 MW; BD696437 CRC32;

Query Match
Best Local Similarity 45.6%; Score 2244; DB 1; Length 1023;
Matches 372; Conservative 202; Mismatches 209; Indels 32; Gaps 27;

Db 39 KQAGCKLLIYPKDYQAST--GSSNDLVKAAEALGIEVHRSEKNGTALAKELFGTTEKL 96

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11 KTGAKKIILYIPQYQYDEQGLQDLVRAAEELGIEVQREERNNTAQTSLGTIOTA 70
97 LGFSERGIALFAPOFDKLLKNKOKLSKLSGSSALGQRLNKTOTALSALQSFLGTAIAG 156
71 IGLTERGIVLSAPOIDKLQKT-KAGQALG-SAESIVQNAKAKTVLSGTSILGSVLG 128
157 MDLSDLLRRRNGEDVSGSELAKAGVLAQALVDNITASATGTVDAFAEOLGKLAMPYLT 216
129 MDLDEALQNSN-OH---A-LAKAGLELTNSLIENIANSVKTLDEFGQEQISQFGSKLQNI 183
217 -ALSGLASKLNNLPDLSPGPGDAVSGIISLVVSASPILSKNDKADAGTKAAAGTEISTKI 275
184 KGLGTGLDKLKNIGGLDKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELANQV 243
276 LGNTGKAVSYIIAQRVAAGLSTTAATGGIIGSVVALAISPLSFLNVADKFERAKOLEQY 335
244 VGNITKAVSYIIAQRVAAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESY 303
336 SERFKEGYEGSDLSASFRETGAIERAALTINSVLSAASAGVGAATGSLVGAPVAALV 395
304 AERFKLGYDGNLALBYQGTGTIDASVTAINTALAAGVSAAGSVIASPIALLV 363
396 SAITGIISGLDASKQAFIRFVATKLANKIDWEKK-HGKNYFENGVDARHSFAFLETFE 454
364 SGITGVSTILOYSQAMFHVANKINKIVEKKNHGNKYNFENGVDARYLANLQDNMK 423
455 LLSQYNKEYSVRVATTOQRWDVNGELAGITRKADAKSGKAYVDFEFGKLLERKDPD 514
424 FLNLNKLQAEVIAITOOQWNNIGDLAGISRLGEKVLSGRAYVDAPEEGKHI-K-AD 481
515 RFDKVVDPLEKIDLSINKT-TL-LKFTIPVPTAGEEIRERKQTKYEMTELFVKKG 572
482 KLVO--LDSANGIIDVNSGAKAKTOHILFTPLTPGTEHRERVQTKYETIKLNINRV 539
573 EKVVVTGESHNAIYDVTNLIQ-LAID-KK-GE-K-ROYTIESHLGKNDRIYLSGSS 626
540 DSWKITDGA--SSTFDLTNNVQRIIGIELDNAGNVTKEKIKIAGLEGEDNDFVFGSGT 598
627 IVYAGNHVDVAYDKTGYLTFDGQSAKAGEYIVTKELKADVKVLYKVVYKTDQISVGK 686
599 EIDGEGYDRVHSRNGYALTDATKETEQGSYTVNRVETG-KALHEVTSHTALVGN 657
687 TCSKLEYRYEYLSFPELNGIRAKDELHVSVEELIGSNRKDKFGSFTDIFHGAKGDDE 746
658 R-EKEIYRSHN-NQHAGY-Y-TKDTLKAVEEIIGTSHNDIFKGSFNDFAFGGCGVDT 713
747 IYNGDGHILYDGDNDVINGGNDHVLGGNGDRLIGGKGN-FLN-GDGDGDELQVF 804
714 IDGNDGNDRLFGGKGDIDLGNGDDFIDGKGNLHGGKGDIFVHRKGDGNDIITDS 773
805 EGOYNVLLGAG-NDILYSGDGNLFDGGVGNDKI 838
774 DGNKLSFSDSNLKDITFEKVKNHLVITNSKKEV 808

RESULT 13
ID RTIL-ACPL STANDARD; PRT; 1023 AA.
AC P55128;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE RTX-I TOXIN DETERMINANT A FROM SEROTYPES 1/9 (APX-IA) (HEMOLYSIN IA)
DE (HLY-IA) (CYTOLYSIN IA) (CLY-IA).
GN APXIA OR CLYIA OR HLYIA.
OS ACTINOBACILLUS PLEUROPNEUMONIAE (HAEMOPHILUS PLEUROPNEUMONIAE).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-S 4074 / SEROTYPE 1;
RX MEDLINE; 91348845.
RA FREY J., MEIER R., GYGI D., NICOLET J.;
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RL INFECT. IMMUN. 59:3026-3032(1991).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN-S 4074 / SEROTYPE 1;
RX MEDLINE; 94237497.
RA FREY J., HALDMANN A., NICOLET J., BOFFINI A., PRENTKI P.;
RL GENE 142:97-102(1994).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
RX MEDLINE; 93366425.
RA JANSEN R., BRIARE J., KAMP E.M., GIELKENS A.L.J., SMITS M.A.;
RL INFECT. IMMUN. 61:3688-3695(1993).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN-S 4074 / SEROTYPE 1;
RA CHANG Y., WANG Y., CHIN N.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,
WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR
ALVEOLAR MACROPHAGES AND NEUTROPHILS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7, 8, 12, AND
TOTALLY DELETED IN SEROTYPE 3.
CC -!- THE SEQUENCE SHOWN IS THAT OF SEROTYPE 1.
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
STRUCTURAL TOXIN).
EMBL; X52899; G38950; -
DR EMBL; X68595; G505570; -
DR EMBL; X73117; G312899; -
DR EMBL; U05042; G606616; -
DR PROSITE; PS00330; HEMOLYSIN-CALCIUM; 2.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 226 256 POTENTIAL.
FT TRANSMEM 297 326 POTENTIAL.
FT TRANSMEM 367 406 POTENTIAL.
FT DOMAIN 722 845 13 X REPEATS, GLY-RICH.
FT REPEAT 722 727 1.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 813 818 10.
FT REPEAT 822 827 11.
FT REPEAT 831 836 12.
FT REPEAT 840 845 13.
FT CONFLICT 210 217 AMPYLTA -> GNALSNT (IN REF. 3 AND 4).
FT CONFLICT 374 374 R -> A (IN REF. 3 AND 4).
FT CONFLICT 562 562 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 687 688 TC -> R (IN REF. 3 AND 4).
SQ SEQUENCE 1023 AA; 110193 MW; 7F21E8E8 CRC32;
Query Match 36.0%; Score 2236; DB 1; Length 1023;
Best Local Similarity 45.5%; Pred. No. 0.00e+00;
Matches 371; Conservative 203; Mismatches 209; Indels 32; Gaps 27;
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Db 39 KQAGQKLIILYIPQYQYQAST--GSSLNDLVKAAEALGIEVHRSEKNTALAKELFGTTEKL 96
QY 11 KTGAKKIILYIPQYQYDEQGLQDLVRAAEELGIEVQREERNNTAQTSLGTIOTA 70
Db 97 LGFSERGIALFAPOFDKLLKNKOKLSKLSGSSALGQRLNKTOTALSALQSFLGTAIAG 156
QY 71 IGLTERGIVLSAPOIDKLQKT-KAGQALG-SAESIVQNAKAKTVLSGTSILGSVLG 128
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Db 157 MDLSDLLRRRRNGEDYSGSELAKAGVDLAQLVDNLTASATGTVDAFAEOLGKLAMPYLFL 216
QY 129 MDLDELALQNNNSN-OH---A-LAKAGLELTNSLTNSVNTKTLDEFEQISQFSGSLQNI 183
Db 217 -ALSGLAKLNNLPDLSLAGPFGFDVSGILSVYSASFILSNKDADAGTAAAGIEISTKI 275
QY 184 KGLGTGDKLKNKTGGDKAGLGLDVLISGLSGATAALVLADKNASTAKKVGAGFELANOV 243
Db 276 LGNIGKAVSOYIIIAQRAVAGLSTTAATGGLIGSVVLAALISPLSFLNVDAKFERAKOLEY 335
QY 244 VGNITRAVSSYIIIAQRAVAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESY 303
Db 336 SERFKFGYEGDSILLASFRETGAIEAALTINSVLSARSAGVGAATSGLVGAPVAALV 395
QY 304 AERFKLGVGDGNDLLAEYQRTGTIDASVTAINTAALAGGVSAAGSVIASPILV 363
Db 396 SAITGIISGILDASKOAFPRVATKLANKIDWEKK-HGKNFYENGVDARHSAFLEDTFE 454
QY 364 SGITGVISTILOYSKQMEFHVANKHNKIVEKNNHKNFYENGVDARYLANQDNMK 423
Db 455 LLQYNKESYVERVAITQOQWNNIGDLGAGISRLGKVLGKAYVDAFECKHI-K-AD 481
QY 424 FLNLNKLQAEVIAITQOQWNNIGDLGAGISRLGKVLGKAYVDAFECKHI-K-AD 481
Db 515 RPDKVPDPLEGLIDISSINKT-TL-LKFTVPVFTAGEIERKQTKGYQYMTFVKGK 572
QY 482 KLVQ--LDSANGAIDVNSGKAKTQHLPLTGTGTEHRRVQTKGYEYITKLNINRV 539
Db 573 EKWVTVGVSHNAIYDVTNLQ-LAID-KK-GE--K-ROVTIESHGEKNDRIYLSGSS 626
QY 540 DSKWITDGA--STFOLTNVQVIGIELDNAGNVTYTKETKIAGLGEEDNVFVGSQT 598
Db 627 IVYAGNHVDVAYDKTDTGYLTFDGSQAOKAGEIYVTKELKADVKVLEKVTQDISVGK 686
QY 599 EIDGEGYDRVHYSRNGALTDATKETEQQSYTVNRFEVG-KALHEVTSHTALVGN 657
Db 687 TCSEKLEYRDYELSPELNGINRAKDELHVSBEIISGNRDKKFFGSRFTDIFHGAAGDDE 746
QY 658 R-BEKIEYRHSN-NQHHAGY-Y-TKDLKAVEEIIITSHNDIFKSGKFNDAFNGGVDVT 713
Db 747 IYNGDGHILYGGDNDVTHGGDNDHLVGGNGDRLIGGKGN-FLN-GGGDDDELQVF 804
QY 714 IDGNDGNDRLFGKGGDDLDGNGDDFDGNGDNDLHGGKGGDIFVHRKGGDNDIITS 773
Db 805 EGYNYLLGAG-NDILYGSDDGNTLFDGGVGNDKI 838
QY 774 DGNDKLSFSDSNLKDLTFEKKVKNHLVITNSKKEV 808

RESULT 14
ID HLVA-ACVAC STANDARD; PRT: 1050 AA.
AC P16462;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LEUKOTOXIN.
GN LKTA OR LTA.
OS ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS
OS ACTINOMYCETEMCOMITANS).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JP2;
RX MEDLINE; 89359382.
RA LALLY E.T., GOLUB E.E., KIEBA I.R., TAICHMAN N.S., ROSENBLUM J.,
RA ROSENBLUM J.C., GIBSON C.W., DEMUTH D.R.;
RL J. BIOL. CHEM. 264:15451-15456(1989).
CC -!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.ACTINOMYCETEMCOMITANS
CC MIGHT BE A CYTOTOXIN, POSSIBLY THE MEMBRANE-BOUND HEMOLYSIN.
CC -!- SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED OR SECRETED (BY
CC SIMILARITY).

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CC -!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC ACTIVITY.
CC -!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
CC INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
CC -!- DISEASE: ITS TARGET CELL SPECIFICITY IS RESTRICTED TO HUMAN AND
CC SOME NON-HUMAN CELLS OF THE MONOMYELOCTIC LINEAGE.
CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE
CC STRUCTURAL TOXIN).
DR EMBL; M27399; G141834; -.
DR PIR; B34345; B34345.
DR HSSP; P04002; 1ATF.
DR PROSITE; PS00330; HEMOLYSIN_CALCIUM; 5.
KW HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;
KW TRANSMEMBRANE.
FT TRANSMEM 339 359 POTENTIAL.
FT TRANSMEM 408 429 POTENTIAL.
FT TRANSMEM 477 501 POTENTIAL.
FT DOMAIN 722 844 14 X REPEATS, GLY-RICH.
FT REPEAT 722 727 1.
FT REPEAT 731 736 2.
FT REPEAT 740 745 3.
FT REPEAT 749 754 4.
FT REPEAT 758 763 5.
FT REPEAT 767 772 6.
FT REPEAT 776 781 7.
FT REPEAT 785 790 8.
FT REPEAT 794 799 9.
FT REPEAT 803 808 10.
FT REPEAT 812 817 11.
FT REPEAT 821 826 12.
FT REPEAT 830 835 13.
FT REPEAT 839 844 14.
SQ SEQUENCE 1050 AA; 114194 MW; 995A56CB CRC32;

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Query Match 34.9%; Score 2167; DB 1; Length 1050;
Best Local Similarity 45.8%; Pred. No. 0.00e+00;
Matches 368; Conservative 190; Mismatches 212; Indels 34; Gaps 25;

Db 44 KTG-KKLTLYIPKNYK----KGNGLTALIKAAQKLGIEVYHEGKDPALTNGLTNGKL 98
QY 11 KTGAKKIILYIPQNYQYDEQNGLODLVKAEEGLIEVQREERNNTATQTSGLTQTA 70
Db 99 LGLTERGUTLFAPELDKWIQGNKHLNSVSGTGNLTKAIDKVVQSVGLTQLAFLATFSGM 158
QY 71 IGLTERGIVLSAPQIDKLLQTKA--GOALGSAESIVQNAKAKTVLSGILSGILSVLAGM 129
Db 159 DLDALIKARQGNKNTVDYQAKASNLINELIGTISSTNNVDTFSKQNLKGLGALGVK 218
QY 130 DLDEAL---QNNNSN-QHA-LAKAGLELTNSLTENIANSVKTLDEFEQISQFSGKLQNI 184
Db 219 HFGSGDKLKNLPKLGNGYKALSVLSAISALLLANKHADTATKAAAALTNKVL 278
QY 185 GLTGLDKLKNIGLDKAGLGLDVLISGLSGATAALVLADKNASTAKKVGAGFELANOV 244
Db 279 GNIGKAITQYIIAQRVAAAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESY 338
QY 245 GNITKAVSSYIIAQRVAAAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSLESY 304
Db 339 KRFKFGYNGSLLGQFYKNTGIADAATTINTVLSAAGVGAASGLVGAIPGLLVS 398
QY 305 ERFKKGVDGNDLLAEYQRTGTIDASVTAINTAALAGGVSAAGSVIASPILV 364
Db 399 AITSLISILDASKOAVSEHIANOLADKIKAWE-NKYGKNYSENGYDARHSAFLEDSKL 457
QY 365 GITGVISTILOYSKQMEFHVANKHNKIVEKNNHKNFYENGVDARYLANQDNMK 424
Db 458 FNEUREKYYTENILSITQOQWQDRIGELAGITRNGDRIOGSKAYVDYLKKGEELEAKHSDK 517
QY 425 LLNLNKLQAEVIAITQOQWNNIGDLGAGISRLGKVLGKAYVDAFECKHI-K-ADK 482
Db 518 FTQKILDPKGNIDLSGI-KGSTT-LTFLNPLLTAGKEERTQSGKYEFTELKVKRT 575

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CC	CELL FUNCTION.
CC	-!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC	-!- ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.
CC	-!- SUBCELLULAR LOCATION: SECRETED.
CC	-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
CC	ACTIVITY (BY SIMILARITY).
CC	-!- PTM: RELEASED IN A PROCESSED FORM.
CC	-!- SIMILARITY: BELONGS TO CLASS-2 OF ADENYLYL CYCLASES.
DR	EMBL: Y00545; G396666; -
DR	EMBL: X14199; G39732; -
DR	EMBL: A07292; G412231; -
DR	EMBL: A14850; G580668; -
DR	PIR: S00893; OYBRC.
DR	PIR: S09403; S09403.
DR	PROSITE: PS00330; HEMOLYSIN CALCIUM; 5.
KW	LYASE; CAMP SYNTHESIS; ATP-BINDING; HEMOLYSIS; TOXIN; VIRULENCE;
KW	WHOOPING COUGH; CALCIUM-BINDING; REPEAT.
FT	CHAIN 1 312 CALMODULIN-SENSITIVE ADENYLYLATE
FT	CHAIN 313 1706 HEMOLYSIN (BY SIMILARITY TO E.COLI
FT	DOMAIN 1 399 HEMOLYSIN (HYA).
FT	DOMAIN 400 912 A, CATALYTIC.
FT	DOMAIN 913 1656 B, ALA/GLY-RICH.
FT	DOMAIN 1657 1706 C.
FT	NP_BIND 349 356 D, ASP/GLY-RICH.
FT	DOMAIN 913 1610 ATP (POTENTIAL).
FT	REPEAT 913 920 28 X REPEATS, GLY-RICH.
FT	REPEAT 1015 1020 1.
FT	REPEAT 1024 1029 2.
FT	REPEAT 1033 1038 3.
FT	REPEAT 1042 1047 4.
FT	REPEAT 1051 1056 5.
FT	REPEAT 1060 1065 6.
FT	REPEAT 1080 1085 7.
FT	REPEAT 1165 1170 8.
FT	REPEAT 1174 1179 9.
FT	REPEAT 1183 1188 10.
FT	REPEAT 1203 1208 11.
FT	REPEAT 1280 1285 12.
FT	REPEAT 1289 1294 13.
FT	REPEAT 1298 1303 14.
FT	REPEAT 1307 1312 15.
FT	REPEAT 1316 1321 16.
FT	REPEAT 1325 1330 17.
FT	REPEAT 1345 1350 18.
FT	REPEAT 1421 1426 19.
FT	REPEAT 1430 1435 20.
FT	REPEAT 1439 1444 21.
FT	REPEAT 1448 1453 22.
FT	REPEAT 1556 1561 23.
FT	REPEAT 1565 1570 24.
FT	REPEAT 1574 1579 25.
FT	REPEAT 1583 1588 26.
FT	REPEAT 1593 1598 27.
FT	REPEAT 1605 1610 28.
FT	MUTAGEN 188 188 D->E,N,Y,H: LOSS OF ACTIVITY.
FT	MUTAGEN 190 190 D->N,Y,H: LOSS OF ACTIVITY.
FT	MUTAGEN 298 298 H->R,P,L: LOSS OF ACTIVITY.
FT	MUTAGEN 301 301 E->Q,K: LOSS OF ACTIVITY.
SQ	SEQUENCE 1706 AA; 177506 MW; ICE709AA CRC32;
Db	Query Match 14.4%; Score 896; DB 1; Length 1706;
Qy	Best Local Similarity 32.0%; Pred. No. 9.23e-119;
Db	Matches 191; Conservative 165; Mismatches 212; Indels 29; Gaps
Db	530 GGFVAGGAGMALGGGIRAAVGCAGSLTD-DAPAGQAAAGAEIATLTGGTVELASSIAL 5
Qy	197 GGLDAGLGLDVISGLSGATAALVLTADKNASTAKKVGAGFELANQVGNITKAVSSY-I 2
Db	589 ALAAARGVTSGLGVAGAGAGAAAGALAAALSPMEIYGLVQQSHYADOLDKLAQESSAYG 6

QY 256 -LAQ-R-VAAGLSSTGCPVAALIASTVSLAISPLAFAGIADKFNHAKSLESYAERFKKLG 312

Db 649 EGDALLAQLYRDKTAAEGAVAGVSAYLSTVGAASVIAAAASVVGAPVAVVTSLLTGALNG 708

QY 313 DGDNLLAEYQRCGTGTIDASVTAINALAAAGVSAAGSVIASPIALLVSGITGVIST 372

Db 709 ILRGVOOPIIEKLANDYARKI-D-ELGGP-QAYFEKNQARHEQLANSDGLRKMILADLOA 765

QY 373 ILQYSKQAMFEHVANKIHKNKIVWEKNNHGNKYNFENGYDARY--LANQDNMKFLLNLNK 430

Db 766 GWNASSVIGVQTEISKSALAAITGNADNLKSDVDFVDRFVQGERVAGOPVV-LDVAA 824

QY 431 ELQAEVIAITQQQWNNIGDLAGISRLGKVLGKAYVDAFECKHAKDLVQLDSAN 490

Db 825 GGIDIASR-KGERPALFTFTPLAAGEEQRRRTKTKSEFTTFEIVEVGKQDRWRIRDGAA 883

QY 491 GIIDVSNCKAKTQHILFRTPLLTPGTEHRRVQIGKYEYITKLN-IRVDSMKITDGAA 549

Db 884 DTTIDLAKVVSQ-L-VD-AN-G-VLK-HSIKLDVIGDGDVVLANASRIHYDGGAGTNTV 938

QY 550 SSTFDLTNVQRIIGIELDNAGNVTKETKIIAKLGEQDDNVFVSGGTTIEDGGEYDRV 609

Db 939 SYAALGRQDSITVSA--DGER--ENVRKOLNNANYREGVATQTTAYGKRTENVQYRHE 994

QY 610 HYSR-GNYGALTIDATKETEQSSYTVNRFVETGKALHEVTSTHALVGNREEKIEIRHSN 668

Db 995 LARVGQVVEVDLHVQHIIGGAGNDSITGNAHDNFLAGSGGDDRLDGGAGNDTLVGGEG 1054

QY 669 NQHHAGYTKDTLKAVEEIIIGTSHNDIFKGSKFNDAFNGGVDITDGNDRFLFGCKG 728

Db 1055 QNTVIGGAGDDVFLQDLGVSNQLDGGAGVDVYKNVHQPSEERLERMGDTGIHADL 1111

QY 729 DDILDGGNGDD-FIDG-GKGNOLLHGGKG-DDI-F-VHRKGDGN-DIITDSGNDKL 779

Search completed: Wed Dec 9 19:25:32 1998
Job time : 123 secs.

WQELH
(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:25:49 1998; Maspar time 49.79 Seconds
936.191 Million cell updates/sec

Tabular output not generated.

Title: >US-08-455-970-12
Description: (1-936) from US08455970.pep
Perfect Score: 6217
Sequence: 1 MATVIDLSFPKTKAKKILY.....LSSLQFARGSQHWSYGLRPG 936

Scoring table: PAM 150
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 54.486; Variance 138.232; scale 0.394

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Pred. No.	
Result No.	Score	Query Match	Length	ID	Description	
1	2324	37.4	998	2	Q47461	PLASMID-DNA FOR EHEC-H
2	2321	37.3	998	2	Q47462	HEMOLYSIN.
3	2307	37.1	998	2	P71223	EHEC-HEMOLYSIN.
4	2207	35.5	1055	2	Q43892	LEUKOTOXIN.
5	1758	28.3	758	2	Q46716	HLIA (FRAGMENT).
6	1396	22.5	233	2	Q51865	LEUKOTOXIN A (FRAGMENT
7	1247	20.1	211	2	Q51867	LEUKOTOXIN A (FRAGMENT
8	1208	19.4	208	2	Q51868	LEUKOTOXIN A (FRAGMENT
9	1148	18.5	200	2	Q51866	LEUKOTOXIN A (FRAGMENT
10	887	14.3	1705	2	Q05179	ADENYLATE CYCLASE HEMO
11	493	7.9	181	2	Q70070	ALPHA HEMOLYSIN (FRAGM
12	492	7.9	181	2	Q68403	ALPHA HEMOLYSIN (FRAGM
13	492	7.9	181	2	Q68404	ALPHA HEMOLYSIN (FRAGM
14	272	4.4	219	2	P96437	EXPEL.
15	270	4.3	269	2	Q05199	SLYA PROTEIN.
16	225	3.6	322	2	Q44223	HLIA (FRAGMENT).
17	226	3.6	398	2	Q67179	HEMOLYSIN.
18	221	3.6	835	2	Q56012	CELL-SURFACE-ASSOCIATE
19	224	3.6	937	2	Q44492	MANNURONAN C-5-EPIMERA
20	223	3.6	997	2	Q44495	MANNURONAN C-5-EPIMERA

21	226	3.6	1028	2	O68083	POTENTIAL OUTER MEMBRA	3.58e-13
22	217	3.5	591	2	P73019	IRON-REGULATED PROTEIN	5.48e-12
23	218	3.5	643	2	O68085	HYPOTHETICAL 64.2 KD P	4.05e-12
24	211	3.4	1403	2	Q44494	MANNURONAN C-5-EPIMERA	3.31e-11
25	203	3.3	1741	2	P73817	HEMOLYSIN.	3.56e-10
26	200	3.2	646	2	O51813	OSCILLIN.	8.60e-10
27	198	3.2	1839	2	Q44496	MANNURONAN C-5-EPIMERA	1.54e-09
28	189	3.0	958	2	O33527	BACTERIOCIN.	2.10e-08
29	181	2.9	553	2	Q44493	MANNURONAN C-5-EPIMERA	2.06e-07
30	175	2.8	474	2	Q52515	LIPASE.	1.12e-06
31	169	2.7	465	2	O33680	ENDO-1,3-1,4-BETA-GLYC	5.90e-06
32	167	2.7	613	2	O59933	EXTRACELLULAR LIPASE (1.02e-05
33	169	2.7	1771	2	P74647	HYPOTHETICAL 192.2 KD	5.90e-05
34	182	2.6	480	2	O69771	SERRALYSIN PRECURSOR (3.99e-05
35	160	2.6	613	2	O59932	LIPASE (EC 3.1.1.3) (T	6.84e-05
36	164	2.6	1290	2	P74649	LEUKOTOXIN (LTA).	2.32e-05
37	159	2.6	1517	2	O34071	ORF40.	8.95e-05
38	159	2.6	3591	2	O45365	FILAMENTOUS HEMAGGLUTI	8.95e-05
39	156	2.5	272	2	O53085	NODO.	1.99e-04
40	133	2.5	476	2	P72120	ALKALINE PROTEINASE.	4.41e-04
41	148	2.4	834	2	O52647	OUTER MEMBRANE PROTEIN	1.63e-03
42	147	2.4	1361	2	O30524	S-LAYER PROTEIN.	2.11e-03
43	150	2.4	3016	2	P73590	HYPOTHETICAL 311.5 KD	9.69e-04
44	143	2.3	476	2	O66388	METALLOPROTEASE.	5.89e-03
45	135	2.2	999	9	O21882	HYPOTHETICAL 104.5 KD	4.38e-02

ALIGNMENTS

RESULT		1		PRELIMINARY;		PRT;		998 AA.	
ID	Q47461	AC	Q47461	DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE	PLASMID-DNA FOR EHEC-HEMOLYSIN OPERON.	DE	PLASMID-DNA FOR EHEC-HEMOLYSIN OPERON.	GN	EHEC-HLYA.	GN	EHEC-HLYA.	OS	ESCHERICHIA COLI.
OG	PLASMID P0157.	OG	PLASMID P0157.	OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.	OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.	OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
RN	[1]	RN	[1]	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	RC	STRAIN-EDL 933;
RX	MEDLINE; 95172699.	RX	MEDLINE; 95172699.	RA	SCHMIDT H., BEUTIN L., KARCH H.;	RA	SCHMIDT H., BEUTIN L., KARCH H.;	RL	INFECT. IMMUN. 63:1055-1061(1995).
DR	EMBL: X86087; E152893;	DR	EMBL: X86087; E152893;	DR	PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 2.	DR	PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 2.	DR	PFAM; PF00353; hemolysinCbind.
KW	PLASMID.	KW	PLASMID.	SQ	SEQUENCE 998 AA; 107032 MW; 3CCADC38 CRC32;	SQ	SEQUENCE 998 AA; 107032 MW; 3CCADC38 CRC32;	SQ	SEQUENCE 998 AA; 107032 MW; 3CCADC38 CRC32;

Query Match		37.4%;		Score 2324;		DB 2;		Length 998;	
Best Local Similarity		46.9%;		Pred. No. 0.00e+00;					
Matches		368;		Conservative 199;		Mismatches 188;		Indels 29;	
								Gaps 23;	
Db	29	RSAGKKLILLIPNY--EA-QGVGINELYKADELGIEIHRERDQTAITANQFFGAAEKV	85						
Qy	11	KYGAKKILIIYQNYDYTEQNGLDLYKAEELGIEVQREERNIATAQTSGLTIQTA	70						
Db	86	VGTERGVAIFAPQDLKLOKQYKGVSKIGGTAENYGNNGKAGTVLSALQNTFTIALSG	145						
Qy	71	IGLTERGIVLSAPQIDKLLQK-TKAGQALG-SAESIVQNAKRAKTVLSGIOSILGSLVAG	128						
Db	146	MALDELLRQREGEDISQNDIAKSSIETLNLQVDTYSSINSTVDSFSEQLNQLGSLSSK	205						
Qy	129	MDLDEAL--QNNNS-N--QHALAKAGLELNSLIENTANSYKTLDFEGEIQSGSKLQNI	183						
Db	206	PRELSSVGGKQLNQLDGLPLGDGVVSGILSAVSASFILGNSDAHTGTAAAGIELTTOV	265						
Qy	184	KGUGTGLDKLKNIGGLDKAGLDVLSGLLSGATAAVLVADKNASTAKKVGAGFELANQV	243						


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RESULT 8
ID Q51866 PRELIMINARY; PRT; 208 AA.
AC Q51866;
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DE LEUKOTOXIN A (FRAGMENT).
OS PASTEURILLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T4 SEROTYPE;
RA LAISON A.F., AITCHISON K.D., DONACHIE W.;
RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 222885; G311831;
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 1.
DR PFAM: PF00353; hemolysinCabin.
FT NON_TER 1
SQ SEQUENCE 208 AA; 22803 MW; A8C5DB0F CRC32;

Query Match 19.4%; Score 1208; DB 2; Length 208;
Best Local Similarity 82.2%; Pred. No. 1.84e-166;
Matches 171; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

Db 1 GNDRLFGGKDDIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRQGDGNDSDIIESEGNK 60
QY 719 GNDRLFGGKDDIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRQGDGNDSDIIESEGNK 778

Db 61 LSFSDSNLKLTEKVNHLVINTKQKVTIQNWFEAEFAKTIYVATRDKIEEII 120
QY 779 LSFSDSNLKLTEKVNHLVINTKQKVTIQNWFEAEFAKTIYVATRDKIEEII 838

Db 121 GCONGERTSKQVDLEIKGKIDKSDLSQVVDNYQLKYSDASNSLDKLISSASFTS 180
QY 839 GCONGERTSKQVDLEIKGKIDKSDLSQVVDNYQLKYSDASNSLDKLISSASFTS 898

Db 181 SNDSRNVLASPTSMLDPSLSIOFARAA 208
QY 899 SNDSRNVLASPTSMLDPSLSIOFARAA 926

RESULT 9
ID Q51866 PRELIMINARY; PRT; 200 AA.
AC Q51866;
DT 01-NOV-1996 (TREMBREL. 01, CREATED)
DT 01-NOV-1996 (TREMBREL. 01, LAST SEQUENCE UPDATE)
DE LEUKOTOXIN A (FRAGMENT).
OS PASTEURILLA HAEMOLYTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T15 SEROTYPE;
RA LAISON A.F., AITCHISON K.D., DONACHIE W.;
RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 222886; G311827;
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 1.
DR PFAM: PF00353; hemolysinCabin.
FT NON_TER 1
SQ SEQUENCE 200 AA; 21986 MW; 172FA6E4 CRC32;

Query Match 18.5%; Score 1148; DB 2; Length 200;
Best Local Similarity 81.5%; Pred. No. 1.21e-156;
Matches 163; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

Db 1 KGGDIIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRQGDGNDSDIIESEGNKLSFSDSNL 60
QY 727 KGGDIIIDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRQGDGNDSDIIESEGNKLSFSDSNL 786

Db 61 KDLTFEKNVHLVINTKQKVTIQNWFEAEFAKTIYVATRDKIEEIIQNGERIT 120
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QY 787 KDLTFEKNVHLVINTKQKVTIQNWFEAEFAKTIYVATRDKIEEIIQNGERIT 846
Db 121 SKQVDLEIKGKIDKSDLSQVVDNYQLKYSDASNSLDKLISSASFTSNDSDRNVL 180
QY 847 SKQVDLEIKGKIDKSDLSQVVDNYQLKYSDASNSLDKLISSASFTSNDSDRNVL 906
Db 181 ASPTSMLDPSLSIOFARAA 200
QY 907 VAPTSMLDPSLSIOFARAA 926

RESULT 10
ID Q05179 PRELIMINARY; PRT; 1705 AA.
AC Q05179;
DT 01-JUL-1997 (TREMBREL. 04, CREATED)
DT 01-JUL-1997 (TREMBREL. 04, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE ADENYLATE CYCLASE HEMOLYSIN.
GN CYAA.
OS BORDETELLA BRONCHISEPTICA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC ALCALIGENACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CIP 9.73;
RX MEDLINE: 96009899.
RA BETSOU F., SIMEIRO O., DANCHIN A., GUISSO N.;
RL GENE 162:165-166(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CIP 9.73;
RA DANCHIN A.;
RL SUBMITTED (SEP-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CIP 9.73;
RA DANCHIN A.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: 237112; E310699;
DR PROSITE: PS00330; HEMOLYSIN_CALCIIUM; 4.
DR PFAM: PF00353; hemolysinCabin.
SQ SEQUENCE 1705 AA; 177249 MW; 452163B0 CRC32;
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Query Match 14.3%; Score 887; DB 2; Length 1705;
Best Local Similarity 31.8%; Pred. No. 2.99e-114;
Matches 190; Conservative 165; Mismatches 212; Indels 30; Gaps 27;

Db 530 GFGVAGGAWALCGGI-GAVGAGMSLTD-DAPAGQAAAGAEIALQITGGTVELASSIAL 587
QY 197 GGLDKAGLGDVIGSLGATAALVLADKNASTAKKVGAGFELANOVVGNITKAVSSY-I 255
Db 588 ALAAARGVTSLQVAGASAGAAALAAALSPMEIYGLVQSHVADQDLKLAOESSAYG 647
QY 256 -LAQ-R-VAAGLSSTGFVAAIATVSLALSLAFIAGIADKFNHAKSLSYAERFKLGY 312
Db 648 EGDALLAQLYRDKTAEGAVAGYSAVLSTVGAASVIAAASVYVAVVYVYVYVYVYVYV 707
QY 313 DGDNLLAEYQRGITDASVTAINTALAAATAGGVSAAAAGSVIATALLVSGITGVIST 372
Db 708 ILRGVQVQPIIEKLANDYARKI-D-ELGGP-QAYFEKNLQARHEOLANSOGLRMLADLQA 764
QY 373 ILQYSKQAMPEHVANKIHNKIVEWKNHNGKNYFENGIDARY--LANLDQNMKFLNLNK 430
Db 765 GWASSVIGVQTTEISKSALEALATGNADNLKASDVVDVFIOGERVAGQPVV-LDVAA 823
QY 431 ELQAEVIAITQQQWNNIGDLAGISRLGKVLGSKRAYVDFAEEGRHKIKADKLVQLDSAN 490
Db 824 GGDIASR-KGERPALTFITPLAAPGEEQRRRTKTKGSEFTTFEIVGKQDRWRIRGAA 882
QY 491 GIIDVNSGRKAKTHILFRPLTPTGTEHREVRVQTKYEYITKLNINRVDKWKITDGA 549
Db 883 DTTIDLAKVYSQL-VD-AN-G-VLK-HSILEKIVGGDDVVLANASRIHVDGAGNTV 937
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Search completed: Wed Dec 9 19:30:04 1998
Job time : 255 secs.

W A R E H
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:30:22 1998; MasPar time 10.01 Seconds
Tabular output not generated. 661.729 Million cell updates/sec

Title: >US-08-455-970-12
Description: (1-936) from US08455970.pep
Perfect Score: 6217
Sequence: 1 MATVIDLSFPRKTGAKKILY.....LSSLQFARGSOHWSYGLRPG 936

Scoring table: PAM 150
Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5-COMB 2:PCT9-COMB 3:backfiles1

Statistics: Mean 34.902; Variance 201.135; scale 0.174

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	6217	100.0	936	1 US-08-455-Sequence 12, Applicati
2	6217	100.0	977	1 US-08-387-Sequence 8, Applicatio
3	6135	98.7	1069	1 US-07-777-Sequence 9, Applicatio
4	6135	98.7	1069	1 US-08-170-Sequence 4, Applicatio
5	6128	98.6	926	3 5476657-3 Patent No. 5476657.
6	6128	98.6	926	1 US-08-387-Sequence 6, Applicatio
7	6128	98.6	926	1 US-07-908-Sequence 2, Applicatio
8	6128	98.6	926	1 US-08-455-Sequence 2, Applicatio
9	6128	98.6	943	1 US-08-455-Sequence 10, Applicati
10	6128	98.6	951	1 US-08-455-Sequence 14, Applicati
11	6057	97.4	1098	1 US-08-170-Sequence 2, Applicatio
12	6057	97.4	1098	1 US-07-777-Sequence 7, Applicatio
13	4925	79.2	934	1 US-08-215-Sequence 80, Applicatio
14	2566	41.3	1244	2 PCT-US93-1 Sequence 2, Applicatio
15	2239	36.0	544	1 US-08-387-Sequence 10, Applicati
16	2167	34.9	1403	1 US-07-908-Sequence 3, Applicatio
17	1758	28.3	1334	3 5476657-1 Patent No. 5476657.
18	1758	28.3	758	1 US-08-258-Sequence 2, Applicatio
19	1758	28.3	758	1 US-08-526-Sequence 2, Applicatio
20	896	14.4	1489	3 PCT-US95-0 Sequence 2, Applicatio
21	896	14.4	1794	3 5183745-2 Patent No. 5183745.
22	896	14.4	1794	3 5183745-6 Patent No. 5183745.
23	160	2.6	613	1 US-08-272-Sequence 3, Applicatio

24	140	2.3	20	3	5476657-6	Patent No. 5476657.	2.07e-01
25	140	2.3	20	1	US-07-908-Sequence 5, Applicatio	Sequence 5, Applicatio	2.07e-01
26	140	2.3	20	1	US-07-777-Sequence 4, Applicatio	Sequence 4, Applicatio	2.07e-01
27	140	2.3	20	1	US-08-170-Sequence 6, Applicatio	Sequence 6, Applicatio	2.07e-01
28	133	2.1	1536	1	US-08-302-Sequence 2, Applicatio	Sequence 2, Applicatio	5.44e-01
29	133	2.1	1536	1	US-08-038-Sequence 2, Applicatio	Sequence 2, Applicatio	5.44e-01
30	133	2.1	2035	1	US-08-393-Sequence 5, Applicatio	Sequence 5, Applicatio	5.44e-01
31	133	2.1	2035	2	PCT-US93-1 Sequence 5, Applicatio	Sequence 5, Applicatio	5.44e-01
32	133	2.1	2035	1	US-08-046-Sequence 7, Applicatio	Sequence 7, Applicatio	5.44e-01
33	133	2.0	1026	1	US-08-194-Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
34	119	1.9	341	1	US-08-062-Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
35	119	1.9	341	2	PCT-US94-0 Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
36	119	1.9	341	1	US-08-891-Sequence 5, Applicatio	Sequence 5, Applicatio	3.63e+00
37	119	1.9	341	2	PCT-US96-0 Sequence 2, Applicatio	Sequence 2, Applicatio	4.73e+00
38	117	1.9	433	1	US-07-661-Sequence 3, Applicatio	Sequence 3, Applicatio	1.19e+01
39	110	1.8	230	1	US-08-118-Sequence 5, Applicatio	Sequence 5, Applicatio	8.03e+00
40	113	1.8	730	1	US-07-845-Sequence 5, Applicatio	Sequence 5, Applicatio	8.03e+00
41	113	1.8	730	1	US-07-846-Sequence 15, Applicati	Sequence 15, Applicati	2.00e+01
42	106	1.7	37	1	US-08-446-Sequence 78, Applicatio	Sequence 78, Applicatio	2.27e+01
43	105	1.7	572	1	US-07-609-Sequence 6, Applicatio	Sequence 6, Applicatio	2.27e+01
44	105	1.7	572	1	US-08-765-Sequence 2, Applicatio	Sequence 2, Applicatio	1.75e+01
45	107	1.7	746	2	PCT-US95-1 Sequence 2, Applicatio	Sequence 2, Applicatio	1.75e+01

ALIGNMENTS

RESULT 1
ID US-08-455-970A-12 STANDARD; PRT; 936 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 12, Application US/08455970A
XX
CC Sequence 12, Application US/08455970A
CC Patent No. 5708155
CC GENERAL INFORMATION:
CC APPLICANT: POTTER, ANDREW A.
CC APPLICANT: REDMOND, MARK J.
CC APPLICANT: HUGHES, HUW P.A.
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
CC TITLE OF INVENTION: CHIMERAS
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: REED & ROBINS
CC STREET: 285 HAMILTON AVENUE, SUITE 200
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: UNITED STATES OF AMERICA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/455,970A
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.10
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3400
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 936 amino acids

CC	TYPE: amino acid	Query Match	100.08;	Score 6217;	DB 1;	Length 936;
CC	TOPOLOGY: linear	Best Local Similarity	100.08;	Pred. No. 0.00e+00;		
CC	MOLECULE TYPE: protein	Matches 936;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
SEQ	SEQUENCE	936 AA;	100529 MW;	4311495 CN;		
Db	1	MATVIDLSFPKTKAKKIILYIPQNYQYDTEQGNGLQDLYKAAEELGIEVQREERNIIATA	60			
Qy	1	MATVIDLSFPKTKAKKIILYIPQNYQYDTEQGNGLQDLYKAAEELGIEVQREERNIIATA	60			
Db	61	QTSLGTTQTALGTERGIVLSAPQIDKLLOKTKAGALGSAESIVONAKAKTVLSGIGS	120			
Qy	61	QTSLGTTQTALGTERGIVLSAPQIDKLLOKTKAGALGSAESIVONAKAKTVLSGIGS	120			
Db	121	ILGSVLGAMDLDEALQNNSHQALAKAGLELTNSLIENTANSVKTLDEFGQISQFGSKL	180			
Qy	121	ILGSVLGAMDLDEALQNNSHQALAKAGLELTNSLIENTANSVKTLDEFGQISQFGSKL	180			
Db	181	QNIKGLGTGLDKLKNIGGLDKAGLDGDIVISGLSGATAALVLADKNASTAKKYGAGFELA	240			
Qy	181	QNIKGLGTGLDKLKNIGGLDKAGLDGDIVISGLSGATAALVLADKNASTAKKYGAGFELA	240			
Db	241	NOVVGNITTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL	300			
Qy	241	NOVVGNITTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL	300			
Db	301	ESVAERFKKLGCDGNDLLAEYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA	360			
Qy	301	ESVAERFKKLGCDGNDLLAEYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA	360			
Db	361	LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVVEKNNHKNYFENG YDARYLANLOD	420			
Qy	361	LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVVEKNNHKNYFENG YDARYLANLOD	420			
Db	421	NMFELNLNLQELQAEVIAITQQQDNNIGDLAGISRLGEKVLGSKAYYDADFEGKHIIKA	480			
Qy	421	NMFELNLNLQELQAEVIAITQQQDNNIGDLAGISRLGEKVLGSKAYYDADFEGKHIIKA	480			
Db	481	DKLVQDLSANGIIDVNSGKAKTQHILFRPLITPGTEHREVRVOTGKYEITKLINLRVD	540			
Qy	481	DKLVQDLSANGIIDVNSGKAKTQHILFRPLITPGTEHREVRVOTGKYEITKLINLRVD	540			
Db	541	SWKITDGAASSTFDLTNVVQRI GIELDNAGNVTKTKETKIIAKLGBGDDNVFVGSGTTEI	600			
Qy	541	SWKITDGAASSTFDLTNVVQRI GIELDNAGNVTKTKETKIIAKLGBGDDNVFVGSGTTEI	600			
Db	601	DGGEGYDRVHSRGNYGALTI DATKETEQGSYTVNRFEVETGKALHEVTSHTTALVGNREE	660			
Qy	601	DGGEGYDRVHSRGNYGALTI DATKETEQGSYTVNRFEVETGKALHEVTSHTTALVGNREE	660			
Db	661	KIEYRHSNNQHHAGYYTKDLKVAVEEIIIGTSHNDIFKGSKFNDAFNGGCGVDITDGN	720			
Qy	661	KIEYRHSNNQHHAGYYTKDLKVAVEEIIIGTSHNDIFKGSKFNDAFNGGCGVDITDGN	720			
Db	721	DRLFGGKGDIDLGNGGDDFDGKGNDLLHGGKGGDDIFVHRKGDNDNIITDSDGNDKLS	780			
Qy	721	DRLFGGKGDIDLGNGGDDFDGKGNDLLHGGKGGDDIFVHRKGDNDNIITDSDGNDKLS	780			
Db	781	FDSNLKDLTFEYKVKHNLVITNSKKEVTIQNFRADFAKEVPNYKATKDEKIEIIGQ	840			
Qy	781	FDSNLKDLTFEYKVKHNLVITNSKKEVTIQNFRADFAKEVPNYKATKDEKIEIIGQ	840			
Db	841	NGERITSQKVQDDLIAGKNGKITQDELSKVVYDNTVELLKHKNVTVNSLDKLISSYSAFTSSN	900			
Qy	841	NGERITSQKVQDDLIAGKNGKITQDELSKVVYDNTVELLKHKNVTVNSLDKLISSYSAFTSSN	900			
Db	901	DSRNLVAPVTSMLDQSLSSIQFARGSHWSYGLRPG	936			
Qy	901	DSRNLVAPVTSMLDQSLSSIQFARGSHWSYGLRPG	936			

QY 181 QNTKGLTGLDKLKNIGGLDKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVVGNTTKAVSSYIIAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300
QY 241 NOVVGNTTKAVSSYIIAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300
Db 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAIAAGGVSAAAAGSVIASPIA 360
QY 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAIAAGGVSAAAAGSVIASPIA 360
Db 361 LLYSGITGVISTILQYSKQAMFEHVANKIHKNIVEKNHGNKYPFNGYDARYLANLQD 420
QY 361 LLYSGITGVISTILQYSKQAMFEHVANKIHKNIVEKNHGNKYPFNGYDARYLANLQD 420
Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLSGKAYVDAPFEGHKA 480
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLSGKAYVDAPFEGHKA 480
Db 481 DKLVQDLSANGIIDVNSGKAKTQHILFRPLTTPGTEHRRVOTGKYEYITKLINRVD 540
QY 481 DKLVQDLSANGIIDVNSGKAKTQHILFRPLTTPGTEHRRVOTGKYEYITKLINRVD 540
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDAGNAGNVTKTKETKIIAKLGECDNNVFGSGTTEI 600
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDAGNAGNVTKTKETKIIAKLGECDNNVFGSGTTEI 600
Db 601 DGEGYDRVHYSRGNYGALTIDATKETEQQSGSYTVNRFVETGKALHEVTSTHTALVGNREE 660
QY 601 DGEGYDRVHYSRGNYGALTIDATKETEQQSGSYTVNRFVETGKALHEVTSTHTALVGNREE 660
Db 661 KIEVRHNNHAGYYTKDTLKAVEELIGTSHNDIFKGSKFNDAFNGDGVDTIDGNDGN 720
QY 661 KIEVRHNNHAGYYTKDTLKAVEELIGTSHNDIFKGSKFNDAFNGDGVDTIDGNDGN 720
Db 721 DRLFGGKDDILDGNGDDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780
QY 721 DRLFGGKDDILDGNGDDDFIDGGKNDLLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780
Db 781 FSDSNLKDITFEKVKHNLVTNSKKEKVTIONWFREADFAPKVPNYKATKDEKIEEIGQ 840
QY 781 FSDSNLKDITFEKVKHNLVTNSKKEKVTIONWFREADFAPKVPNYKATKDEKIEEIGQ 840
Db 841 NGERITSQVDDLLAKNGKITODELSKVVDNYELLKHSKNVTNSLDKLSSVSFTSSN 900
QY 841 NGERITSQVDDLLAKNGKITODELSKVVDNYELLKHSKNVTNSLDKLSSVSFTSSN 900
Db 901 DSRNLVAPTSMLDQSLSSQLQFARGSQHWSYGLRPG 936
QY 901 DSRNLVAPTSMLDQSLSSQLQFARGSQHWSYGLRPG 936

RESULT 3
ID US-07-777-715-9 STANDARD: PRT; 1069 AA.
XX
AC
XX
XX

Sequence 9, Application US/07777715
Patent No. 5273889
GENERAL INFORMATION:
CC APPLICANT: Potter, Andrew
CC APPLICANT: Campos, Manuel
CC APPLICANT: Hughes, Huw P. A.
CC TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND
CC TITLE OF INVENTION: USES THEREOF
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Morrison & Foerster
CC STREET: 545 Middlefield Road, Suite 200
CC CITY: Menlo Park

CC STATE: California
CC COUNTRY: USA
CC ZIP: 94025
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/777.715
CC FILING DATE: 19911016
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 29310-2001320
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-327-7250
CC TELEFAX: 415-327-2951
CC TELEX: 706141
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1069 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1069 AA; 116205 MW; 5591501 CN;
Query Match 98.7%; Score 6135; DB 1; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSPFKTGAKKIILYIPONYQYDTEQNGLDLVKAAAEELGIEVQREERNIATA 60
QY 1 MATVIDLSPFKTGAKKIILYIPONYQYDTEQNGLDLVKAAAEELGIEVQREERNIATA 60
Db 61 QTSLGITQIATIGTERGIVLSAPOIDKLLQKTKAGALGSAESIVQNANKAKTVLSGIQS 120
QY 61 QTSLGITQIATIGTERGIVLSAPOIDKLLQKTKAGALGSAESIVQNANKAKTVLSGIQS 120
Db 121 ILGSLVAGMDLDELALQNNNSQHALAKAGLELTNSLIENTANSVKTLDGEQEQISQFGSKL 180
QY 121 ILGSLVAGMDLDELALQNNNSQHALAKAGLELTNSLIENTANSVKTLDGEQEQISQFGSKL 180
Db 181 QNTKGLTGLDKLKNIGGLDKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNTKGLTGLDKLKNIGGLDKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVVGNTTKAVSSYIIAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300
QY 241 NOVVGNTTKAVSSYIIAQRVAAGLSTGTPVAALIASTVSLAISPAPAGIADTFENHAKSL 300
Db 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAIAAGGVSAAAAGSVIASPIA 360
QY 301 ESVAERFKLGYDGDNLAEYQRTGTIDASVTAINATAAIAAGGVSAAAAGSVIASPIA 360
Db 361 LLYSGITGVISTILQYSKQAMFEHVANKIHKNIVEKNHGNKYPFNGYDARYLANLQD 420
QY 361 LLYSGITGVISTILQYSKQAMFEHVANKIHKNIVEKNHGNKYPFNGYDARYLANLQD 420
Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLSGKAYVDAPFEGHKA 480
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLSGKAYVDAPFEGHKA 480
Db 481 DKLVQDLSANGIIDVNSGKAKTQHILFRPLTTPGTEHRRVOTGKYEYITKLINRVD 540
QY 481 DKLVQDLSANGIIDVNSGKAKTQHILFRPLTTPGTEHRRVOTGKYEYITKLINRVD 540
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDAGNAGNVTKTKETKIIAKLGECDNNVFGSGTTEI 600
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDAGNAGNVTKTKETKIIAKLGECDNNVFGSGTTEI 600
Db 601 DGEGYDRVHYSRGNYGALTIDATKETEQQSGSYTVNRFVETGKALHEVTSTHTALVGNREE 660

QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEAGSYVNRFEVETGKALHEVTSHTALVGNREE 660
 Db 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSKFNDAFNGGVDVTIDGNDGN 720
 QY 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSKFNDAFNGGVDVTIDGNDGN 720
 Db 721 DRLFGKGDDIILDGNGDDFIDGGKNDLLHGGKGGDIFVHRKGGDNDIITSDGNDKLS 780
 QY 721 DRLFGKGDDIILDGNGDDFIDGGKNDLLHGGKGGDIFVHRKGGDNDIITSDGNDKLS 780
 Db 781 FSDSNLKDITFEKVKNLVTINSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 QY 781 FSDSNLKDITFEKVKNLVTINSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 Db 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
 QY 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
 Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927
 QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927

RESULT 4
 ID US-08-170-126-4 STANDARD; PRT: 1069 AA.

XX AC xxxxxx

Sequence 4, Application US/08170126

Sequence 4, Application US/08170126
 Patent No. 5594107

GENERAL INFORMATION:
 CC APPLICANT: POTTER, ANDREW
 CC APPLICANT: CAMPOS, MANUEL
 CC APPLICANT: HUGHES, HUW P.A.
 CC TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES
 CC TITLE OF INVENTION: THEREOF
 CC NUMBER OF SEQUENCES: 6
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: REED & ROBINS
 CC STREET: 635 BRYANT STREET
 CC CITY: PALO ALTO
 CC STATE: CALIFORNIA
 CC COUNTRY: UNITED STATES OF AMERICA
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/170.126
 CC FILING DATE: 20-DEC-1993
 CC CLASSIFICATION: 530
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/777,715
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/571,301
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: ROBINS, ROBERTA L.
 CC REGISTRATION NUMBER: 33,208
 CC REFERENCE/DOCKET NUMBER: 9000-0013.21
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 617-8999
 CC TELEFAX: (415) 327-3231
 CC INFORMATION FOR SEQ ID NO: 4:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 1069 amino acids
 CC TYPE: amino acid

CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 1069 AA; 116205 MW; 5591501 CN;
 Query Match 98.7%; Score 6135; DB 1; Length 1069;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MATVIDLSFPKGTAKKIIILYIPQNYQYDTEQNGQLDVLKAAEELGIEVQREERNIIATA 60
 QY 1 MATVIDLSFPKGTAKKIIILYIPQNYQYDTEQNGQLDVLKAAEELGIEVQREERNIIATA 60
 Db 61 QTSLGITQATGLTERGIVLSAPQIDKLLQTKAQOALGSAESIVQNAKANKATVLSGTS 120
 QY 61 QTSLGITQATGLTERGIVLSAPQIDKLLQTKAQOALGSAESIVQNAKANKATVLSGTS 120
 Db 121 ILGSLVLAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEQISQFGSKL 180
 QY 121 ILGSLVLAGMDLDEALQNNNSQHALAKAGLELTNSLIENIANSVKTLDFEQISQFGSKL 180
 Db 181 QNIKGLGTGLDKLKNIGGLDRAKGLDVISGLLGATAALVLADKNASTAKKVGAGFELA 240
 QY 181 QNIKGLGTGLDKLKNIGGLDRAKGLDVISGLLGATAALVLADKNASTAKKVGAGFELA 240
 Db 241 NOVVGNIITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFHAKSL 300
 QY 241 NOVVGNIITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFHAKSL 300
 Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAGSVIASPIA 360
 QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAGSVIASPIA 360
 Db 361 LLVSGITGVISTILOYSKOAMFEHVANKIHKNIVEWKNHGNKYNFYENGIDARYLANLQD 420
 QY 361 LLVSGITGVISTILOYSKOAMFEHVANKIHKNIVEWKNHGNKYNFYENGIDARYLANLQD 420
 Db 421 NMKFLNLNKLQAEERVAITQQQWDNIGDLAGISRLGKESVLSKAYVDAFEKHKHKA 480
 QY 421 NMKFLNLNKLQAEERVAITQQQWDNIGDLAGISRLGKESVLSKAYVDAFEKHKHKA 480
 Db 481 DKLVLDSANGIIDVNSGKAKTQHILFPTLLTPGTEHRRVQTKYEYITKLNINRVD 540
 QY 481 DKLVLDSANGIIDVNSGKAKTQHILFPTLLTPGTEHRRVQTKYEYITKLNINRVD 540
 Db 541 SWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETIIAKLGEEDDNVFGSGTTEI 600
 QY 541 SWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETIIAKLGEEDDNVFGSGTTEI 600
 Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEAGSYVNRFEVETGKALHEVTSHTALVGNREE 660
 QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEAGSYVNRFEVETGKALHEVTSHTALVGNREE 660
 Db 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSKFNDAFNGGVDVTIDGNDGN 720
 QY 661 KIEYRHSNNQHAGYYTKDTLKAVEEIICTSHNDIFKSKFNDAFNGGVDVTIDGNDGN 720
 Db 721 DRLFGKGDDIILDGNGDDFIDGGKNDLLHGGKGGDIFVHRKGGDNDIITSDGNDKLS 780
 QY 721 DRLFGKGDDIILDGNGDDFIDGGKNDLLHGGKGGDIFVHRKGGDNDIITSDGNDKLS 780
 Db 781 FSDSNLKDITFEKVKNLVTINSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 QY 781 FSDSNLKDITFEKVKNLVTINSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 Db 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
 QY 841 NGERITSKQVDDLIAGNGKITQDELSKYVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
 Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927
 QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQ 927

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RESULT 5
ID 5476657-3 STANDARD: PRT: 1003 AA.
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AC xxxxxx
XX
DT 01-JAN-1900
DE
XX
DE Patent No. 5476657.
XX
XX Patent No. 5476657
CC
CC APPLICANT: POTTER, ANDREW A.
CC TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN
CC COMPOSITIONS AND USES THEREOF
CC NUMBER OF SEQUENCES: 8
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/15,537
CC FILING DATE: 09-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 504,850
CC FILING DATE: 05-APR-1990
CC APPLICATION NUMBER: 335,018
CC FILING DATE: 07-APR-1989
CC
CC SEQ ID NO:3:
CC LENGTH: 926
CC
CC SEQUENCE 1003 AA; 107828 MW; 5444703 CN;

Query Match 98.6%; Score 6128; DB 3; Length 926;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 ILGSLVAGMDLDEALQNNQSHALAKAGLELTNSLIENIANSVKTLDFEFGESIQSGSKL 180
QY 121 ILGSLVAGMDLDEALQNNQSHALAKAGLELTNSLIENIANSVKTLDFEFGESIQSGSKL 180

Db 181 QNKGGLTGLGDKNIGLQKAGLGLDVISGLLSGATAALVLADKNASTAKVKGAGFELA 240
QY 181 QNKGGLTGLGDKNIGLQKAGLGLDVISGLLSGATAALVLADKNASTAKVKGAGFELA 240

Db 241 NOVVGNTTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVVGNTTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300

Db 301 ESYAERFKKLGVDGNLLAEYQRTGTIDASVTAINALAAIAGVSAAGSIVIASPIA 360
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Db 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIYEWKNNHKNYFENGVDARYLANLQD 420
QY 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIYEWKNNHKNYFENGVDARYLANLQD 420

Db 421 NMKFLNLLNKLQEAERVIAITQQQMDNNGIDLAGISRLGERKVLGSKAYVDAFEESKHKA 480
QY 421 NMKFLNLLNKLQEAERVIAITQQQMDNNGIDLAGISRLGERKVLGSKAYVDAFEESKHKA 480

Db 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLTPGTEHREVRVOTGKYEYITKLNINRVD 540
QY 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLTPGTEHREVRVOTGKYEYITKLNINRVD 540

Db 541 SWKITDGAASSTFDLTNNVQRIIGELDNAGNVTKTKETKIIAKLGEEDNVFVSGGTETI 600
QY 541 SWKITDGAASSTFDLTNNVQRIIGELDNAGNVTKTKETKIIAKLGEEDNVFVSGGTETI 600

Db 601 DGGEGYDRVHYSRGNYGALTIDATKETBOGSYTVNRFVETGKALHEVTSHTALVGNREE 660
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETBOGSYTVNRFVETGKALHEVTSHTALVGNREE 660

661 KIEYRHSNNQHHAGYYTKDTLKAVEEIIIGTSHNDIFKSGKFNDAFNGDGVDTIDGNDGN 720
QY 661 KIEYRHSNNQHHAGYYTKDTLKAVEEIIIGTSHNDIFKSGKFNDAFNGDGVDTIDGNDGN 720

721 DRLFGGKGGDDILDGGNGDDFIDGGKGNDDLHGKGGDDIFVHRKGGDNDIITDSGNDKLS 780
QY 721 DRLFGGKGGDDILDGGNGDDFIDGGKGNDDLHGKGGDDIFVHRKGGDNDIITDSGNDKLS 780

781 FDSNKLKDLTFFEKVKHNLVITNSKKEKVTIQNWFRADFAKEVPNKATKDEKIEEIIQ 840
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841 NGRITRSKQVDDLIAGKNGKITODELSKVVDNYELKHKSNVTNSLDKLSSVSFTSSN 900
QY 841 NGRITRSKQVDDLIAGKNGKITODELSKVVDNYELKHKSNVTNSLDKLSSVSFTSSN 900

901 DSRNVLVAPTSMLDQSLSSIQFARGS 926
QY 901 DSRNVLVAPTSMLDQSLSSIQFARGS 926

RESULT 6
ID US-08-387-156-6 STANDARD: PRT: 926 AA.
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AC xxxxxx
XX
DT
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XX
DE Sequence 6, Application US/08387156
XX
XX Sequence 6, Application US/08387156
CC
CC Patent No. 5723129
CC
CC GENERAL INFORMATION:
CC APPLICANT: POTTER, ANDREW A.
CC APPLICANT: REDMOND, MARK J.
CC APPLICANT: HUGHES, HUW P.A.
CC TITLE OF INVENTION: GBRH-LEUKOTOXIN CHIMERAS
CC NUMBER OF SEQUENCES: 28
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: REED & ROBINS
CC STREET: 635 BRYANT STREET
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: UNITED STATES OF AMERICA
CC ZIP: 94301
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/387,156
CC FILING DATE: 10-FEB-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/779,171
CC FILING DATE: 16-OCT-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.21
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 926 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
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QY 301 ESYAERFKKLGVDNLLAEYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
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QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVVEKNHGNKYNFENGVDARYLANLOD 420
Db 421 NMKFLNLNKLKELQAEVIAITQQQWNNIGDLAGISRLGKELVSGRAYVDFAEEGKHKA 480
QY 421 NMKFLNLNKLKELQAEVIAITQQQWNNIGDLAGISRLGKELVSGRAYVDFAEEGKHKA 480
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QY 481 DKLVLQDSANGIIDVSNKAKTQHILFRTPLTPTGTEHRVOTGKYEYITKLNINRVD 540
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDAGISRLGKELVSGRAYVDFAEEGKHKA 600
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDAGISRLGKELVSGRAYVDFAEEGKHKA 600
Db 601 DKGEGYDRVHYSRGNKALIDATKETEQQSYTVNRFVETGKALHEVTSTHTALVGNREE 660
QY 601 DKGEGYDRVHYSRGNKALIDATKETEQQSYTVNRFVETGKALHEVTSTHTALVGNREE 660
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QY 661 KIEYRHSNNQHHAGYTKDTLKAVEEIICTSHNDIFKGSKFNDAGNGDGVDTIDGNDGN 720
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QY 721 DRLFPGKGDDILDGGNGDDIFDGGKNDLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780
Db 781 FDSNLKDLTFEKVKNLVTNSKKKVTIQNMFREADFAPKPNYKATKDEKIEELIGQ 840
QY 781 FDSNLKDLTFEKVKNLVTNSKKKVTIQNMFREADFAPKPNYKATKDEKIEELIGQ 840
Db 841 NGERITSQVDDLIAGKNGRITQDELKSVYDNYELLKHSKNVNSLDKLISVSAFTSSN 900
QY 841 NGERITSQVDDLIAGKNGRITQDELKSVYDNYELLKHSKNVNSLDKLISVSAFTSSN 900
Db 901 DSRNLVAPTSMLDQSLSSLOFARGS 926
QY 901 DSRNLVAPTSMLDQSLSSLOFARGS 926

RESULT 8
ID US-08-455-970A-2 STANDARD: PRT: 926 AA.

AC xxxxxx

Sequence 2, Application US/08455970A

Sequence 2, Application US/08455970A

Patent No. 5708155

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN

TITLE OF INVENTION: CHIMERAS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 HAMILTON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/455,970A
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.10
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3400
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 926 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 926 AA: 99346 MW; 4207190 CN;

Query Match 98.6%; Score 6128; DB 1; Length 926;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSPKTKGAKKILYIPQNYQYDTEQNGQLQDLVKAEEELGIEVQREERNIATA 60
QY 1 MATVIDLSPKTKGAKKILYIPQNYQYDTEQNGQLQDLVKAEEELGIEVQREERNIATA 60
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QY 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELNSLIENIANSVKTLDFEGEIQISQFGSKL 180
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QY 181 QNTKGLGTIGDKLKNITGGDLKAGLDVTSGLLSGATAALVLADKNASTAKKVAGFELA 240
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QY 301 ESYAERFKKLGVDNLLAEYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
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QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVVEKNHGNKYNFENGVDARYLANLOD 420
Db 421 NMKFLNLNKLKELQAEVIAITQQQWNNIGDLAGISRLGKELVSGRAYVDFAEEGKHKA 480
QY 421 NMKFLNLNKLKELQAEVIAITQQQWNNIGDLAGISRLGKELVSGRAYVDFAEEGKHKA 480
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QY 481 DKLVLQDSANGIIDVSNKAKTQHILFRTPLTPTGTEHRVOTGKYEYITKLNINRVD 540
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QY 541 SWKITDGAASSTFDLTNNVQRIEGLDAGISRLGKELVSGRAYVDFAEEGKHKA 600
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QY 601 DKGEGYDRVHYSRGNKALIDATKETEQQSYTVNRFVETGKALHEVTSTHTALVGNREE 660
Db 661 KIEYRHSNNQHHAGYTKDTLKAVEEIICTSHNDIFKGSKFNDAGNGDGVDTIDGNDGN 720
QY 661 KIEYRHSNNQHHAGYTKDTLKAVEEIICTSHNDIFKGSKFNDAGNGDGVDTIDGNDGN 720

Db 721 DRLFGGKDDIILDDGGDDDFIDGGKGNLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780
QY 721 DRLFGGKDDIILDDGGDDDFIDGGKGNLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780
Db 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQ 840
QY 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQ 840
Db 841 NGERITSKQVDDLLAKNGKIIQDELKSIVVDNYELLKHSKNVTNSLDKLISVSFAFTSSN 900
QY 841 NGERITSKQVDDLLAKNGKIIQDELKSIVVDNYELLKHSKNVTNSLDKLISVSFAFTSSN 900
Db 901 DSRNVLVAPTSMLDQSLSLQFARG 926
QY 901 DSRNVLVAPTSMLDQSLSLQFARG 926
RESULT 9
ID US-08-455-970A-10 STANDARD: PRT: 943 AA.
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AC xxxxxx
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DT
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DE
XX
CC Sequence 10, Application US/08455970A
CC Sequence 10, Application US/08455970A
CC Patent No. 5708155
CC GENERAL INFORMATION:
CC APPLICANT: POTTER, ANDREW A.
CC APPLICANT: REDMOND, MARK J.
CC APPLICANT: HUGHES, HUI P.A.
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: REED & ROBINS
CC STREET: 285 HAMILTON AVENUE, SUITE 200
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: UNITED STATES OF AMERICA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08455,970A
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.10
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3400
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 943 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 943 AA: 101229 MW: 4397993 CN:
Query Match 98.6%; Score 6128; DB 1; Length 943;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEQNGQLDVLVKAEEELGIEVQREERNIATA 60
QY 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEQNGQLDVLVKAEEELGIEVQREERNIATA 60
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QY 181 QNIRKGLTFLGDKLNIGLDRKAGLGLDVISGLLGATAALVLADKNASTAKKVGAGEFLA 240
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QY 361 LLVSGITGVISTILQYSKQAMFEHVANKHNKIVWEKNNHGNFYFENGVDARYLANLQD 420
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QY 421 NKVELLNKELQAEVITATQOQWDDNNIGDLAGISRLGKVLGSKAYVDAFEGKHIKA 480
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QY 481 DKLVLQDSANGIIDVSNRGAKTQHILFRPLTPGTEHRRVOTKYEYITKLNINRVD 540
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QY 601 DGGGYDRVHYSRGNYGALTIDATKETEQGSYTVNRVETGKALHEVTSTHTALVGNREE 660
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QY 721 DRLFGGKDDIILDDGGDDDFIDGGKGNLHGGKDDIFVHRKGDGNDIITDSGNDKLS 780
Db 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQ 840
QY 781 FDSNLKDLTFFKVKHNLVITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQ 840
Db 841 NGERITSKQVDDLLAKNGKIIQDELKSIVVDNYELLKHSKNVTNSLDKLISVSFAFTSSN 900
QY 841 NGERITSKQVDDLLAKNGKIIQDELKSIVVDNYELLKHSKNVTNSLDKLISVSFAFTSSN 900
Db 901 DSRNVLVAPTSMLDQSLSLQFARG 926
QY 901 DSRNVLVAPTSMLDQSLSLQFARG 926
RESULT 10
ID US-08-455-970A-14 STANDARD: PRT: 951 AA.
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AC xxxxxx
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CC FILING DATE: 20-DEC-1993
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/777,715
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/571,301
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9000-0013.21
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1098 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1098 AA: 118577 MW: 5903750 CN:
SQ

Query Match 97.4%; Score 6057; DB 1; Length 1098;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 183 KTGAKKIILYIPONYQYDTEQNGLDLVKAAEELGIEVOREERNNIATAQSLGTIQT 242
QY 11 KTGAKKIILYIPONYQYDTEQNGLDLVKAAEELGIEVOREERNNIATAQSLGTIQT 70

Db 243 IGLTERGIVLSAPOIDKLQTKAGALGSAESIVONANKAKTVLSGIOSILGSLVLAGMD 302
QY 71 IGLTERGIVLSAPOIDKLQTKAGALGSAESIVONANKAKTVLSGIOSILGSLVLAGMD 130

Db 303 LDEALQNNQHAKARAGLELTNSLIENIANSYKTLDEFGEQISQFGSKLQNIKGLGTIG 362
QY 131 LDEALQNNQHAKARAGLELTNSLIENIANSYKTLDEFGEQISQFGSKLQNIKGLGTIG 190

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QY 191 DLKNTGGDLKAGLDVLSGLSGATAALVLADKNASTAKKVGAGFELANQVGNITKA 250

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Db 483 GYDGDNLLAEYQRTGTIDASVTAINALAAIAGGVSAAAGSVIASPIALLVSGITGYI 542
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Db 603 ELQAEVIAITOOQDNNIGDLAGISRLGKVLGSKAYYDAFEKGHIKADKLVLQDLSAN 662
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Db 663 GIIDVNSGKAKTQHILFRPLTLPCTGHEHRRVQTKYEYITKLNINRVDSWKITDGAAS 722
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Db 723 STFDLTNVQVIGIELDNAGNVTKTETKIIAKLGGEDDNVFGSGTTTIDGEGYDRVH 782
QY 551 STFDLTNVQVIGIELDNAGNVTKTETKIIAKLGGEDDNVFGSGTTTIDGEGYDRVH 610

Db 783 YSRGNYGALTIDATKETEQSYTVNREVTGKALHEVTSHTHALVGNREEKTEYRHSNQ 842
QY 611 YSRGNYGALTIDATKETEQSYTVNREVTGKALHEVTSHTHALVGNREEKTEYRHSNQ 670

Db 843 HHAGYTKDTLKAVEEIICTSHNDIFKGSKFNDAFNGDGVDTIDGNDGNRLFGGKGDD 902
QY 671 HHAGYTKDTLKAVEEIICTSHNDIFKGSKFNDAFNGDGVDTIDGNDGNRLFGGKGDD 730

Db 903 ILDGGNGDDFIDGGKGNLHGGKGDDIFVHRKGGDNDIITDSGDNKLSFSDSNLKDLT 962
QY 731 ILDGGNGDDFIDGGKGNLHGGKGDDIFVHRKGGDNDIITDSGDNKLSFSDSNLKDLT 790

Db 963 FEKVHNLVITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQGGERITSQV 1022
QY 791 FEKVHNLVITNSKKEKVTIQNWFEADFAKEVPYKATKDEKIEEIIQGGERITSQV 850

Db 1023 DDLIAKGNGKITQDELKSVVDNYELLKHKSNVTNSLKLISVSFTSSNDSRNVLVAPT 1082
QY 851 DDLIAKGNGKITQDELKSVVDNYELLKHKSNVTNSLKLISVSFTSSNDSRNVLVAPT 910

Db 1083 SMLDOSLSLQFARG 1098
QY 911 SMLDOSLSLQFARG 926

RESULT 12
ID US-07-777-715-7 STANDARD; PRT; 1098 AA.
XX
AC xxxxxx
XX
DT
XX
XX
DE Sequence 7, Application US/07777715
XX
CC Sequence 7, Application US/07777715
CC Patent No. 5273889
CC GENERAL INFORMATION:
CC APPLICANT: Potter, Andrew
CC APPLICANT: Campos, Manuel
CC APPLICANT: Hughes, Huw P.A.
CC TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND
CC TITLE OF INVENTION: USES THEREOF
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Morrison & Foerster
CC STREET: 545 Middlefield Road, Suite 200
CC CITY: Menlo Park
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94025
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/777,715
CC FILING DATE: 19911016
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 29310-2001320
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-327-7250
CC TELEFAX: 415-327-2951
CC TELEX: 706141
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1098 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1098 AA: 118577 MW: 5903750 CN;
SQ

Query Match 97.4%; Score 6057; DB 1; Length 1098;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 183 KTGAKKIILYIPONYQYDTEQNGLDLVKAAEELGIEVOREERNNIATAQSLGTIQT 242

QY 11 KTGAKKIILYIPQNYDYDEQNGLODLVKAAREELGIEVQREERNNIATQTSLSGTIQT 70
Db 243 IGLTERGIVLSAPOIDKLLQKTAGQALGSAESIVONANKAKTVLSGIIOSILGSLVLAGMD 302
QY 71 IGLTERGIVLSAPOIDKLLQKTAGQALGSAESIVONANKAKTVLSGIIOSILGSLVLAGMD 130
Db 303 LDALQNNNSOHALAKAGLELNSLTENTANSVKTLDGEQISQFGSKLQNIKGLGTLG 362
QY 131 LDALQNNNSOHALAKAGLELNSLTENTANSVKTLDGEQISQFGSKLQNIKGLGTLG 190
Db 363 DKLKNIIGGLDKAGLDVIGSLGSLGATAALVLADKNASTAKKVGAGFELANQVGVNITKA 422
QY 191 DKLKNIIGGLDKAGLDVIGSLGSLGATAALVLADKNASTAKKVGAGFELANQVGVNITKA 250
Db 423 VSSYILAQVAGLSSTGPVVAALIASTVSLAISPLAFAGIADKFNNAKLSAESYAEFRKL 482
QY 251 VSSYILAQVAGLSSTGPVVAALIASTVSLAISPLAFAGIADKFNNAKLSAESYAEFRKL 310
Db 483 GYDGDNLAEYORGTGTIDASVTANTALAAATAGGVSAAGSVIASPALLVSGITGYI 542
QY 311 GYDGDNLAEYORGTGTIDASVTANTALAAATAGGVSAAGSVIASPALLVSGITGYI 370
Db 543 STILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGVDARYLANLQDNMKFLNLNK 602
QY 371 STILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGVDARYLANLQDNMKFLNLNK 430
Db 603 ELQAEVIAITQOQWNNIGDLGASIRLGEKVLGSKAYVDAFEEGKHIRKADKLVLQDLSAN 662
QY 431 ELQAEVIAITQOQWNNIGDLGASIRLGEKVLGSKAYVDAFEEGKHIRKADKLVLQDLSAN 490
Db 663 GIIDVNSGKAKTOHLFRTPLTPGTEHRRVQTKYKYEITKLNINRVDSWKITDGAAS 722
QY 491 GIIDVNSGKAKTOHLFRTPLTPGTEHRRVQTKYKYEITKLNINRVDSWKITDGAAS 550
Db 723 STFDLNVVQIRIGIELDNAGNVTKTETKIIAKLGGDDNVFVSGTTEIDGEGYDRVH 782
QY 551 STFDLNVVQIRIGIELDNAGNVTKTETKIIAKLGGDDNVFVSGTTEIDGEGYDRVH 610
Db 783 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 842
QY 611 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 670
Db 843 HHAGYVTKDILKAVEIIGTSHNDIFKSGFNDAFNGDGDVDTIDGNDGNRLFGKGDD 902
QY 671 HHAGYVTKDILKAVEIIGTSHNDIFKSGFNDAFNGDGDVDTIDGNDGNRLFGKGDD 730
Db 903 ILDGGNGDDFIDGGKNDLLHGGKGDDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDLT 962
QY 731 ILDGGNGDDFIDGGKNDLLHGGKGDDIFVHRKGGDNDIITDSGNDKLSFSDSNLKDLT 790
Db 963 FEKVHNLVITNSKKEKVTIQNWFREADFAKEVPNYKATKDEKIEEIIQNGERITSKV 1022
QY 791 FEKVHNLVITNSKKEKVTIQNWFREADFAKEVPNYKATKDEKIEEIIQNGERITSKV 850
Db 1023 DDLIANGNKITODELSKVVDNYELLKHSKNVTNSDLKLISVSATSSNDNRNLVAPT 1082
QY 851 DDLIANGNKITODELSKVVDNYELLKHSKNVTNSDLKLISVSATSSNDNRNLVAPT 910
Db 1083 SMLDQSLSSLOFARGS 1098
QY 911 SMLDQSLSSLOFARGS 926

RESULT 13

ID US-08-215-805A-80 STANDARD; PRG; 934 AA.

XX AC xxxxxx

XX DT

XX DE

XX Sequence 80, Application US/08215805A

XX Sequence 80, Application US/08215805A

CC Patent No. 5559008
CC GENERAL INFORMATION:
CC APPLICANT: Chang, Yung-Fu
CC TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURELLA
CC TITLE OF INVENTION: SUIS
CC NUMBER OF SEQUENCES: 84
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nixon, Hargrave, Devans & Doyle
CC STREET: Clinton Square, P.O. Box 1051
CC CITY: Rochester
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 14603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA: US/08/215,805A
CC APPLICATION NUMBER: US/08/215,805A
CC FILING DATE: 22-MAR-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Timian, Susan J.
CC REGISTRATION NUMBER: 34,103
CC REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (716) 263-1636
CC TELEFAX: (716) 263-1600
CC INFORMATION FOR SEQ ID NO: 80:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 934 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: Pasteurella suis
CC STRAIN: 5943
CC IMMEDIATE SOURCE:
CC LIBRARY: P. suis DNA in Bacteriophage lambda-dash
CC CLONE: (Lambda)7fc33-37
CC SEQUENCE 934 AA; 100477 MW; 4245576 CN;

Query Match 79.2%; Score 4925; DB 1; Length 934;

Best Local Similarity 79.8%; Pred. No. 0.00e+00;

Matches 705; Conservative 112; Mismatches 66; Indels 1; Gaps 1;

Db 34 KAGAKKILYIPKDYDSGRNGIQLDVLKAAEDLGIEVQREERNGIATAQNSLTIQNI 93
QY 11 KTGAKKIILYIPQNYDYDEQNGLODLVKAAREELGIEVQREERNNIATQTSLSGTIQT 70
Db 94 LGFSRGVLSAPOIDKLLQKTAGQALGSAESIVONANKAKTVLSGIIOSILGSLVLAGMD 153
QY 71 IGLTERGIVLSAPOIDKLLQKTAGQALGSAESIVONANKAKTVLSGIIOSILGSLVLAGMD 130
Db 154 LDEILKNKSELDLAKAGLELNSLTENTANSVKTLDGEQISQFGSKLQNIKGLGTLG 213
QY 131 LDEALQNNNSOHALAKAGLELNSLTENTANSVKTLDGEQISQFGSKLQNIKGLGTLG 190
Db 214 DKLKNIIGGLDKAGLDVIGSLGSLGATAALVLADKNASTAKKVGAGFELANQVGVNITKA 273
QY 191 DKLKNIIGGLDKAGLDVIGSLGSLGATAALVLADKNASTAKKVGAGFELANQVGVNITKA 250
Db 274 VSSYILAQVAGLSSTGPVVAALIASTVSLAISPLAFAGIADKFNNAKLSAESYAEFRKL 333
QY 251 VSSYILAQVAGLSSTGPVVAALIASTVSLAISPLAFAGIADKFNNAKLSAESYAEFRKL 310
Db 334 GYDGDNLAEYORGTGTIDASVTANTALAAATAGGVSAAGSVIASPALLVSGITGYI 393
QY 311 GYDGDNLAEYORGTGTIDASVTANTALAAATAGGVSAAGSVIASPALLVSGITGYI 370
Db 394 STILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGVDARYLANLQDNMKFLNLNK 453

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|||||
QY 371 STILOYSQAMFEHVANKIHNKIVKWEKNNHKNFYNGYDARYLANQDNKFLNLNK 430
Db 454 ELQAEVIRITQOQNDNIGNLAGISRLGKVMKSKAYADAFEEGKLKADTFVOLDSAT 513
QY 431 ELQAEVIRITQOQNDNIGNLAGISRLGKVMKSKAYADAFEEGKLKADTFVOLDSAT 490
Db 514 GVINTSKSDNVKTHILFRTPLLTGTVNRRRIQTKGVEYITKLNINRVDSWKKITDGN 573
QY 491 GIIDVNSGKAKTOHILFRTPLLTGTEHREVRVOTGKVEYITKLNINRVDSWKKITDGAAS 550
Db 574 STFDLTNNVQVIGIELDHADNVTKETKIILANLGDGNDVFIQSGTTEVDGNGDLRVH 633
QY 551 STFDLTNNVQVIGIELDHADNVTKETKIILAKLGEEDNVFVSGTTEIDGGEYDRVH 610
Db 634 YSRGDYALTIDATNESVQGSYTVKRFVETGKALHEVTATQSVLVGSREEKIEYRHSNNT 693
QY 611 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYRHSNQ 670
Db 694 QHAGYTTDTLKSVEEIICTSRNDIFKSKFDADAFHGGDGVNDIDGNAGNDRLFGGKGF 753
QY 671 HHAGYTTDTLKAVEEIICTSHNDIFKSKFNDAFNGDGVDTIDGNDGNDRLFGGKGD 730
Db 754 IIDGGDGDFFIDGGOGDILHGGKNDILCTVKG-GNDSISDSGNDRLSPADSNLKDLT 812
QY 731 ILDGGGDDFFIDGGKNDLLHGGKDDIFVIRKGDGNDIITDSGNDKLSFSDSNLKDLT 790
Db 813 FEKVNHMLITNVKKEKTYIQNWFEADYAKTVHNYQATADEKIEEIIIGROGERITSKQI 872
QY 791 FEKVHNLVITNSKKEKTYIQNWFEADYAKTVHNYQATADEKIEEIIIGROGERITSKQV 850
Db 873 DELIEKGGKIDQSELERIARSSALLKSKFASNLKLVSSAA 916
QY 851 DDLIAGKNGKITQDLSKVDVNDYELKSKHKNVTNSLDKLISSVS 894

RESULT 14
ID .PCT-US93-10500-2 STANDARD: PRT: 1244 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 2, Application PC/TUS9310500
Sequence 2, Application PC/TUS9310500
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: Recombinant Vaccine For Procine
TITLE OF INVENTION: Pleuropneumoniae
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Alan S. Korman
CITY: Buffalo
STATE: New York
COUNTRY: U.S.A.
ZIP: 14202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10500
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/972,229
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Korman, Alan S.
REGISTRATION NUMBER: 33,932
```

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REFERENCE/DOCKET NUMBER: 19603/00001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-853-8104
TELEFAX: 716-853-8109
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1244 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
STRAIN: Serotypes 2, 3, 4, 6 and 8
INDIVIDUAL ISOLATE: Swine
CELL TYPE: Gram negative bacterium
SQ SEQUENCE 1244 AA; 135397 MW; 7631235 CN;

Query Match 41.3%; Score 2566; DB 2; Length 1244;
Best Local Similarity 52.2%; Pred. No. 6.12e-178;
Matches 401; Conservative 177; Mismatches 167; Indels 23; Gaps 20;

Db 228 GNKLVVIP-K-EYDGSVGVGFFDLVKAEEELGIQVYVNRNEVAHSLGTADQPLGL 285
QY 14 AKRIILYIPONYQYDEQGNLQDLVKAEEELGIEVQREERNIATAQTSLGTIQTALG 73
Db 286 TERGLTFAFOLQFLOKHSKISNVVGSSTGDVASKLAKSQTIIISGSIQSVLGTVLGINL 345
QY 74 TERGIVLSAPQIDKLLQK-TRAGOALGSABES-IVONANKAKTIVLSGIQSILGSVLGMDL 131
Db 346 NEAIISSGSELELAEGVSLASELVNSIAKGTITIDAFITQIONFG-KLAENAKGLGVG 404
QY 132 DEALQNNNQHALAKAGLELTNSLIENIANSVKTLDFEGEIQISQFGSKL-QNIKGLGLT 190
Db 405 RQONISGSALSKTGLDIISSLLSGVTRSFALRNKNASTSTKVAAGFELSNOVIGIT 464
QY 191 DKLKNIGG--LDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELANQVVGNI 248
Db 465 KAVSSYILAORLAGLSTTGPAALIASISLAISPLAFLRVADNFRSKEIGEFARFK 524
QY 249 KAVSSYILAORVAGLSSTGPVAAIATVSLAISPLAFAGIADKFNHAKLSLESYARFK 308
Db 525 KLGVDGDKLSEFYHEAGTIDASTITISALSAIAGTAASAGALYGPITLLVTGITG 584
QY 309 KLGVDGNLLAEYQRGTTIDASTVTAINTALAAAGVSAAGSVIASPIALLVSGITG 368
Db 585 LISGILEFSKQPMLDHVASKIGNKIDWEKK-YGKNYFENGYPARHAKAFLEDSEFSLSSF 643
QY 369 VISTILOYSQAMFEHVANKIHNKIVKWEKNNHKNFYNGYDARYLANQDNKFLNL 428
Db 644 NKQYETERAVLITQORWDEYIGELAGITGKDKLSSGKAYVDYFQEGKLEKPPDFSKV 703
QY 429 NKLQAEVIRITQOQNDNIGNLAGISRLGKVMKSKAYADAFEEGKHI--KADKL--V 484
Db 704 VFDPTEKIDISNS-QTSTL-LKFVTPLLTPGPTESRETRTQTKGYEYITKLVKVGKQWV 761
QY 485 QLDOSANGIIDVNSGKAKTOHILFRTPLLTGTEHREVRVOTGKVEYITKLNINRVDSWKI 544
Db 762 NGVKDGAVYDYNLIQHAHIS-SSVARGEEYREVLVSHLGNNGNDKVFLLAAGSAEIHAG 820
QY 545 TDGAA-SSTFDLTNNVQVIGIELDHADNVTKETKIILAKLGEEDNVFVSGTTEIDGG 603
Db 821 EGHVYVYDKTDGLVIDGKTATGEGRYSVTRFELSCATKILREVINKQYKAVKKEETL 880
QY 604 EGYDRVHYSRGNYGALTIDATKETEQGSYTVNR-FVETGKALHEVTSHTFALVGNREEKI 662
Db 881 EYRDYELTQSGNSNLKAHDELHLSVEETI-GSNQDEPKGSRFRDIFHGADGDDLLNGDGD 939
QY 663 EYRHSN-NQH-HAGYTTKDTLKAVEEIICTSHNDIFKSKFNDAFNGDGVDTIDGNDGN 720
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Db 940 DILYDKNDELRCNGNDOLYCGEGDDKLLGGNGNN-YL-SGGDGN 985
QY 721 DRLEGGKDDILDGGNGDDFIDGGKNDLLHGGKGDIDFVHRKGDGND 768

RESULT 15
ID US-08-387-156-10 STANDARD; PRT; 544 AA.
XX xxxxxx

Sequence 10, Application US/08387156

Sequence 10, Application US/08387156

Patent No. 5723129

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

APPLICANT: HUGHES, HUW P.A.

TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 635 BRYANT STREET

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,156

FILING DATE: 10-FEB-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/779,171

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.21

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 544 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 544 AA; 57542 MW; 1502532 CN;

Query Match 36.0%; Score 2239; DB 1; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.35e-153;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKTKGAKKIILYIPQNYQYDEQNGLDLVKAAEELGIEVQREERNIATA 60

QY 1 MATVIDLSFPKTKGAKKIILYIPQNYQYDEQNGLDLVKAAEELGIEVQREERNIATA 60

Db 61 QTSGLTIQTALIGLTERGIVLSAPQIDKLLQTKAGQALGSAESIVQNANKAKTVLSGIQS 120

QY 61 QTSGLTIQTALIGLTERGIVLSAPQIDKLLQTKAGQALGSAESIVQNANKAKTVLSGIQS 120

Db 121 ILGSVLGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDEFFGEQISQFGSKL 180

QY 121 ILGSVLGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDEFFGEQISQFGSKL 180

QY 121 ILGSVLGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDEFFGEQISQFGSKL 180
Db 181 QNIKGLGTLDGDKLKNIGGLDKAGLDVIGLLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNIKGLGTLDGDKLKNIGGLDKAGLDVIGLLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVVGNIITRAVSSYIIAORVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVVGNIITRAVSSYIIAORVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
Db 301 ESYAERFKILGYDGNLLAEYQRTGTIDASVTAINATAAGGVSAAAA 351
QY 301 ESYAERFKILGYDGNLLAEYQRTGTIDASVTAINATAAGGVSAAAA 351

Search completed: Wed Dec 9 19:31:17 1998
Job time : 55 secs.

WQSEFH
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:31:35 1998; MasPar time 45.64 Seconds

Tabular output not generated. 770.326 Million cell updates/sec

Title: >US-08-455-970-12
Description: (1-936) from US08455970.pep
Perfect Score: 6217
Sequence: 1 MATVIDLSFPTGAKKILY.....LSSLFARGSQHWSYGLRPG 936

Scoring table: PAM 150
Gap 11

Searched: 318656 seqs, 37563770 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-pending
1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85
10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP
17:NEWU8 18:NEWU9

Statistics: Mean 38.748; Variance 234.154; scale 0.165

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6217	100.0	936	US-08-455-	Sequence 12, Applicati	0.00e+00
2	6217	100.0	936	US-07-779-	Sequence 10, Applicati	0.00e+00
3	6217	100.0	977	US-09-124-	Sequence 8, Applicati	0.00e+00
4	6217	100.0	977	US-08-594-	Sequence 8, Applicati	0.00e+00
5	6217	100.0	977	US-08-878-	Sequence 2, Applicati	0.00e+00
6	6128	98.6	926	US-08-535-	Sequence 6, Applicati	0.00e+00
7	6128	98.6	926	US-08-694-	Sequence 2, Applicati	0.00e+00
8	6128	98.6	926	US-08-455-	Sequence 2, Applicati	0.00e+00
9	6128	98.6	926	US-08-878-	Sequence 6, Applicati	0.00e+00
10	6128	98.6	926	US-07-779-	Sequence 14, Applicati	0.00e+00
11	6128	98.6	926	US-09-124-	Sequence 6, Applicati	0.00e+00
12	6128	98.6	943	US-08-455-	Sequence 10, Applicati	0.00e+00
13	6128	98.6	943	US-07-779-	Sequence 12, Applicati	0.00e+00
14	6128	98.6	951	US-07-779-	Sequence 8, Applicati	0.00e+00
15	6128	98.6	951	US-08-455-	Sequence 14, Applicati	0.00e+00
16	6117	98.4	924	US-08-619-	Sequence 8, Applicati	0.00e+00
17	6117	98.4	924	US-08-038-	Sequence 8, Applicati	0.00e+00
18	6117	98.4	924	US-08-038-	Sequence 12, Applicati	0.00e+00
19	6117	98.4	924	US-08-038-	Sequence 15, Applicati	0.00e+00
20	4925	79.2	1111	US-07-972-	Sequence 2, Applicati	0.00e+00
21	4925	79.2	1111	US-07-972-	Sequence 2, Applicati	0.00e+00

22 4925 79.2 1111 3 US-07-972- Sequence 2, Applicatio 0.00e+00
23 4254 68.4 956 7 US-08-396- Sequence 8, Applicatio 6.27e-288
24 2566 41.3 1049 7 US-08-396- Sequence 11, Applicati 8.40e-168
25 2566 41.3 1244 4 US-08-072- Sequence 2, Applicatio 2.64e-148
26 2291 36.9 1022 7 US-08-396- Sequence 10, Applicati 1.27e-144
27 2239 36.0 544 15 US-09-124- Sequence 10, Applicati 1.27e-144
28 2239 36.0 544 10 US-08-694- Sequence 10, Applicati 1.27e-144
29 2239 36.0 544 12 US-08-878- Sequence 10, Applicati 1.27e-144
30 2194 35.3 699 15 US-09-124- Sequence 16, Applicati 1.96e-141
31 2194 35.3 699 10 US-08-694- Sequence 16, Applicati 1.96e-141
32 2167 34.9 1403 10 US-08-694- Sequence 17, Applicati 1.60e-139
33 2167 34.9 1403 9 US-08-535- Sequence 3, Applicati 1.60e-139
34 2167 34.9 1403 15 US-09-124- Sequence 17, Applicati 1.60e-139
35 896 14.4 1706 10 US-08-669- Sequence 2, Applicatio 3.02e-50
36 887 14.3 1705 10 US-08-669- Sequence 4, Applicatio 1.27e-49
37 345 5.5 693 3 US-07-972- Sequence 3, Applicatio 7.29e-13
38 345 5.5 693 3 US-07-972- Sequence 3, Applicatio 7.29e-13
39 265 4.3 1115 7 US-08-323- Sequence 2, Applicatio 1.01e-07
40 265 4.3 1115 3 US-07-895- Sequence 2, Applicatio 1.01e-07
41 267 4.3 1382 14 US-09-057- Sequence 4, Applicatio 7.57e-08
42 286 4.3 1857 14 US-09-057- Sequence 2, Applicatio 8.76e-08
43 266 4.3 1805 14 US-09-057- Sequence 7, Applicatio 8.76e-08
44 223 3.6 997 7 US-08-387- Sequence 4, Applicatio 4.26e-05
45 223 3.6 997 7 US-08-387- Sequence 4, Applicatio 4.26e-05

ALIGNMENTS

RESULT 1
ID US-08-455-970-12 STANDARD; PRT; 936 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX

Sequence 12, Application US/08455970

Sequence 12, Application US/08455970

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

APPLICANT: HUGHES, HUW P. A.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN

TITLE OF INVENTION: CHIMERAS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 HAMILTON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970

FILING DATE: 31-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-07/960,932

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 327-3400

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

QY 241 NOVVGNTKAVSSYILAQRVAAGLSTGPVAALIASTVSLAISPFAAGIADKFNHAKSL 300
Db 301 ESYAERFKKLGVDGNLLAAYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
QY 301 ESYAERFKKLGVDGNLLAAYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
Db 361 LLYSGITGVISTILOYSKOAMFEHVANKHNKIVEKNNHKNYFENGVDARYLANLOD 420
QY 361 LLYSGITGVISTILOYSKOAMFEHVANKHNKIVEKNNHKNYFENGVDARYLANLOD 420
Db 421 NMKFLNLNKLQAEVIAITQQOOWDNNIGDLAGISRLGEKVLGSKAYVDFAFEGKHKA 480
QY 421 NMKFLNLNKLQAEVIAITQQOOWDNNIGDLAGISRLGEKVLGSKAYVDFAFEGKHKA 480
Db 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPGTEHRERVOTGKYEYITKLNINRVD 540
QY 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPGTEHRERVOTGKYEYITKLNINRVD 540
Db 541 SWKITDGAASSTFDLTNNVQVIGIELDNAGNVTKTKETKIIAKLGEKDDNVFVSGTTEI 600
QY 541 SWKITDGAASSTFDLTNNVQVIGIELDNAGNVTKTKETKIIAKLGEKDDNVFVSGTTEI 600
Db 601 DGEGYDRVHYSRGNYGALTDATKETEQGSYTVNRFVETGKALHEVYTSHTALVGNREE 660
QY 601 DGEGYDRVHYSRGNYGALTDATKETEQGSYTVNRFVETGKALHEVYTSHTALVGNREE 660
Db 661 KIEYRHSNNQHHAGYTKDTLKAVEEIIIGTSHNDIFKGSKFNDFAFNGGVDITDGNNGN 720
QY 661 KIEYRHSNNQHHAGYTKDTLKAVEEIIIGTSHNDIFKGSKFNDFAFNGGVDITDGNNGN 720
Db 721 DRLFGKGDDILDGGNGDDFIDGGKGNLDLHGKGDDIFVHRKGDGNDIITDSGNDKLS 780
QY 721 DRLFGKGDDILDGGNGDDFIDGGKGNLDLHGKGDDIFVHRKGDGNDIITDSGNDKLS 780
Db 781 FDSNLKDLTFEYKVNHLVITNSKKKERTIQNWFREADFAPKATKDEKIEELIGQ 840
QY 781 FDSNLKDLTFEYKVNHLVITNSKKKERTIQNWFREADFAPKATKDEKIEELIGQ 840
Db 841 NGERITSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVNSLDKLISSVSFTSSN 900
QY 841 NGERITSKQVDDLIAGKNGKITODELSKVVDNYELLKHSKNVNSLDKLISSVSFTSSN 900
Db 901 DSRNLVAPTSMLDQSLSSQLQFARGSOHWSYGLRPG 936
QY 901 DSRNLVAPTSMLDQSLSSQLQFARGSOHWSYGLRPG 936

RESULT 3
ID US-09-124-491-8 STANDARD; PRT; 977 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 8, Application US/09124491
CC Sequence 8, Application US/09124491
CC GENERAL INFORMATION:
CC APPLICANT: POTTER, ANDREW A.
CC APPLICANT: MANNS, JOHN G.
CC TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: REED & ROBINS LLP
CC STREET: 285 HAMILTON AVENUE, SUITE 200
CC CITY: PALO ALTO
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/124,491
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/694,865
CC FILING DATE: 09-AUG-1996
CC APPLICATION NUMBER: US 08/387,156
CC FILING DATE: 10-FEB-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/779,171
CC FILING DATE: 16-OCT-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: MCCracken, THOMAS P.
CC REGISTRATION NUMBER: 38,548
CC REFERENCE/DOCKET NUMBER: 9001-0016.22
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415)327-3400
CC TELEFAX: (415)327-3231
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 977 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 977 AA; 104869 MW; 4761174 CN;
QY

Query Match 100.0%; Score 6217; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSPFKTKAKKILYIPQNYQYDTQOENGLQDLVKAAPFELGIEVQREERNIATA 60
QY 1 MATVIDLSPFKTKAKKILYIPQNYQYDTQOENGLQDLVKAAPFELGIEVQREERNIATA 60
Db 61 QTSLSGTQTAIGLTERGIVLSAPQIDKLQKTAGALGSAESIVQNAKAKTVLSGIQS 120
QY 61 QTSLSGTQTAIGLTERGIVLSAPQIDKLQKTAGALGSAESIVQNAKAKTVLSGIQS 120
Db 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELNTSLNIENTANSVKTLDGEQISQSGSKL 180
QY 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELNTSLNIENTANSVKTLDGEQISQSGSKL 180
Db 181 QNTKGLGTGLDKLNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNTKGLGTGLDKLNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVVGNTKAVSSYILAQRVAAGLSTGPVAALIASTVSLAISPFAAGIADKFNHAKSL 300
QY 241 NOVVGNTKAVSSYILAQRVAAGLSTGPVAALIASTVSLAISPFAAGIADKFNHAKSL 300
Db 301 ESYAERFKKLGVDGNLLAAYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
QY 301 ESYAERFKKLGVDGNLLAAYQRTGTIDASVTAIN TALAAIAGGVSAAAAGSVIASPIA 360
Db 361 LLYSGITGVISTILOYSKOAMFEHVANKHNKIVEKNNHKNYFENGVDARYLANLOD 420
QY 361 LLYSGITGVISTILOYSKOAMFEHVANKHNKIVEKNNHKNYFENGVDARYLANLOD 420
Db 421 NMKFLNLNKLQAEVIAITQQOOWDNNIGDLAGISRLGEKVLGSKAYVDFAFEGKHKA 480
QY 421 NMKFLNLNKLQAEVIAITQQOOWDNNIGDLAGISRLGEKVLGSKAYVDFAFEGKHKA 480
Db 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPGTEHRERVOTGKYEYITKLNINRVD 540
QY 481 DKLVQDLSANGIIDVNSGKAKTQHILFRTPLTPGTEHRERVOTGKYEYITKLNINRVD 540
Db 541 SWKITDGAASSTFDLTNNVQVIGIELDNAGNVTKTKETKIIAKLGEKDDNVFVSGTTEI 600
QY

QY 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNNFVFGSGTTEI 600
 Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQSGSYVNRVETGKALHEVTSHTALVGNREE 660
 QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQSGSYVNRVETGKALHEVTSHTALVGNREE 660
 Db 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720
 QY 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720
 Db 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780
 QY 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780
 Db 781 FSDSNLKDITFEKVHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 QY 781 FSDSNLKDITFEKVHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 Db 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900
 QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900
 Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936
 QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936

RESULT 4

ID US-08-694-865-8 STANDARD; PRG: 977 AA.
 XX
 AC xxxxxx
 CC
 DT

Sequence 8, Application US/08694865

CC Sequence 8, Application US/08694865
 CC GENERAL INFORMATION:
 CC APPLICANT: POTTER, ANDREW A.
 CC TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
 CC NUMBER OF SEQUENCES: 34
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: REED & ROBINS LLP
 CC STREET: 285 HAMILTON AVENUE, SUITE 200
 CC CITY: PALO ALTO
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/694,865
 CC FILING DATE: 09-AUG-1996
 CC CLASSIFICATION: 424
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: MCCracken, THOMAS P.
 CC REGISTRATION NUMBER: 38,548
 CC REFERENCE/DOCKET NUMBER: 9001-0016.22
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415)327-3400
 CC TELEFAX: (415)327-3231
 CC INFORMATION FOR SEQ ID NO: 8:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 977 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 977 AA: 104869 MW: 4761174 CN:

Query Match 100.0%; Score 6217; DB 10; Length 977;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
 QY 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
 Db 61 QTSGLGTIQTALGLTERGVLSAPQIDKLLQTKAQAGLSAESIVONANKAKTVLSGIQS 120
 QY 61 QTSGLGTIQTALGLTERGVLSAPQIDKLLQTKAQAGLSAESIVONANKAKTVLSGIQS 120
 Db 121 ILGSLVAGMDLDEALONNSQHALAKAGLELTNSLIENIANSVKTLDFFGEOISFGSKL 180
 QY 121 ILGSLVAGMDLDEALONNSQHALAKAGLELTNSLIENIANSVKTLDFFGEOISFGSKL 180
 Db 181 QNIKGLGTGKLNIGGLDRAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELA 240
 QY 181 QNIKGLGTGKLNIGGLDRAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELA 240
 Db 241 NOVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFHAKSL 300
 QY 241 NOVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFHAKSL 300
 Db 301 ESYAERFKLGYDGNLLAEYORGTTIDASVTANTALAAIAGGVSAAAGSVIASPIA 360
 QY 301 ESYAERFKLGYDGNLLAEYORGTTIDASVTANTALAAIAGGVSAAAGSVIASPIA 360
 Db 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGYDARYLANIQD 420
 QY 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIVWEKNHGNKYNFENGYDARYLANIQD 420
 Db 421 NMKFLNLNKLQAEVIAITQQQWMDNIGLAGISRLGEKVLGSKAYVDAFECKHIKA 480
 QY 421 NMKFLNLNKLQAEVIAITQQQWMDNIGLAGISRLGEKVLGSKAYVDAFECKHIKA 480
 Db 481 DKLVLDSANGIIDVSNKAKTOHILFRTPLTPTGTEHREVRQTKYEYITKLINRVD 540
 QY 481 DKLVLDSANGIIDVSNKAKTOHILFRTPLTPTGTEHREVRQTKYEYITKLINRVD 540
 Db 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNNFVFGSGTTEI 600
 QY 541 SWKITDGAASSTFDLTNNVQIRIGIELDNAGNVTKTKETKIIAKLGGDDNNFVFGSGTTEI 600
 Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQSGSYVNRVETGKALHEVTSHTALVGNREE 660
 QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQSGSYVNRVETGKALHEVTSHTALVGNREE 660
 Db 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720
 QY 661 KIEYRHSNNQHHAGYTTKTLKAVEEIICTSHNDIFKSGKFNDAFNGGVDYTDIGNDGN 720
 Db 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780
 QY 721 DRLFGKGDDIILDGGNGDDFIDGGKGNLHGGKGGDDIFVHRKGGNDIITDSGNDKLS 780
 Db 781 FSDSNLKDITFEKVHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 QY 781 FSDSNLKDITFEKVHNLVITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 Db 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900
 QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLISVSFTSSN 900
 Db 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936
 QY 901 DSRNVLVAPTSMLDQSLSLQFARGSQHWSYGLRPG 936

RESULT 5
 ID US-08-878-748-8 STANDARD; PRG: 977 AA.
 XX
 AC xxxxxx

QY 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGQALGSAESIVQNANKAKTVLSGIQS 120
Db 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180
QY 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180
Db 181 QNTKGLGTIGDKLKNIGGDKAGLGDDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNTKGLGTIGDKLKNIGGDKAGLGDDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAAGSVIASPIA 360
QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAAGSVIASPIA 360
Db 361 LLYVSGITGVISTILOYSKOAMFEHVANKTHNKIVEKNNHKNYFENGVDARYLANLOD 420
QY 361 LLYVSGITGVISTILOYSKOAMFEHVANKTHNKIVEKNNHKNYFENGVDARYLANLOD 420
Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKRAYVDFAFEGRHKA 480
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKRAYVDFAFEGRHKA 480
Db 481 DKLVQDSANGIIDVNSGKAKTQHILFRPTPLTPTGTEHRRVOTGKYEYITKLNINRVD 540
QY 481 DKLVQDSANGIIDVNSGKAKTQHILFRPTPLTPTGTEHRRVOTGKYEYITKLNINRVD 540
Db 541 SWKITDGAASSTFDLNVVORIGIEDLNAGNVTKTKETKIIAKLGECDNVFVSGTTEI 600
QY 541 SWKITDGAASSTFDLNVVORIGIEDLNAGNVTKTKETKIIAKLGECDNVFVSGTTEI 600
Db 601 DGEGYDRVHYSRGNYGALTDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660
QY 601 DGEGYDRVHYSRGNYGALTDATKETEQGSYTVNRFVETGKALHEVTSHTALVGNREE 660
Db 661 KIEYRSHNNOHAGYTKDTLKAVEEIIIGSHNDIFKGSFNDFAFNGGVDITDGN 720
QY 661 KIEYRSHNNOHAGYTKDTLKAVEEIIIGSHNDIFKGSFNDFAFNGGVDITDGN 720
Db 721 DRLFGKGDDILDGGNGDDFIDGGKNDLHGGKGGDDIFVHRKGDGNDIITDSDGNDKLS 780
QY 721 DRLFGKGDDILDGGNGDDFIDGGKNDLHGGKGGDDIFVHRKGDGNDIITDSDGNDKLS 780
Db 781 FSDSNLKDLTFFERVKHNLVITNSKKEKVTIQNNFREADFAKEVPNYKATKDEKIEELIG 840
QY 781 FSDSNLKDLTFFERVKHNLVITNSKKEKVTIQNNFREADFAKEVPNYKATKDEKIEELIG 840
Db 841 NGERITSKQVDDLIAGKNGKITODELSKVVDNYELLKHKSNVTNSLDKLISSVSFTSSN 900
QY 841 NGERITSKQVDDLIAGKNGKITODELSKVVDNYELLKHKSNVTNSLDKLISSVSFTSSN 900
Db 901 DSRNLVAPTSMLDQSLSSLOFARGS 926
QY 901 DSRNLVAPTSMLDQSLSSLOFARGS 926

RESULT 8
ID US-08-455-970-2 STANDARD: PRT: 926 AA.

XX xxxxxx

XX

DT

XX

DE

XX

CC

CC

CC

CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
CC TITLE OF INVENTION: CHIMERAS
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: REED & ROBINS
CC STREET: 285 HAMILTON AVENUE, SUITE 200
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: UNITED STATES OF AMERICA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/455.970
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960.932
CC FILING DATE: 14-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.10
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3400
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 926 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 926 AA; 99346 MW; 4207190 CN;

Query Match 98.8%; Score 6128; DB 8; Length 926;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSPKTKGAKKILYIPONTYDTEQGNGLDVLKAAEELGIEVQREERNIATA 60
QY 1 MATVIDLSPKTKGAKKILYIPONTYDTEQGNGLDVLKAAEELGIEVQREERNIATA 60
Db 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGQALGSAESIVQNANKAKTVLSGIQS 120
QY 61 QTSLGTTQTAIGLTERGIVLSAPQIDKLLQKTKAGQALGSAESIVQNANKAKTVLSGIQS 120
Db 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180
QY 121 ILGSLVAGMDLDEALQNNNOHALAKAGLELTNSLIENIANSVKTLDGEQISQFGSKL 180
Db 181 QNTKGLGTIGDKLKNIGGDKAGLGDDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240
QY 181 QNTKGLGTIGDKLKNIGGDKAGLGDDVLSGLSGATAALVLADKNASTAKKVGAGFELA 240
Db 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVVGNTKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAAGSVIASPIA 360
QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASVTAINTALAAIAGGVSAAAAGSVIASPIA 360
Db 361 LLYVSGITGVISTILOYSKOAMFEHVANKTHNKIVEKNNHKNYFENGVDARYLANLOD 420
QY 361 LLYVSGITGVISTILOYSKOAMFEHVANKTHNKIVEKNNHKNYFENGVDARYLANLOD 420
Db 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKRAYVDFAFEGRHKA 480
QY 421 NMKFLNLNKLQAEVIAITQQQWNNIGDLAGISRLGEKVLGSKRAYVDFAFEGRHKA 480

Db 481 DKLVLQDSANGIIDVNSGKAKTOHILFRTPLLTGCTEHRERVQTKYEYITKLNINRVD 540
QY 481 DKLVLQDSANGIIDVNSGKAKTOHILFRTPLLTGCTEHRERVQTKYEYITKLNINRVD 540
Db 541 SWKITDGAASSTFDLTNNVQRIEGLDAGNAGVTCTKTKIIAKLGEEDNNVFGSGTTEI 600
QY 541 SWKITDGAASSTFDLTNNVQRIEGLDAGNAGVTCTKTKIIAKLGEEDNNVFGSGTTEI 600
Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRVETGKALHEVTSHTALVGNREE 660
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQGSYTVNRVETGKALHEVTSHTALVGNREE 660
Db 661 KIEYRHSNNQHHAGYVTKDTLKAVEEIIIGTSHNDIFKGSKFENDAFNGGVDVTIDGNDGN 720
QY 661 KIEYRHSNNQHHAGYVTKDTLKAVEEIIIGTSHNDIFKGSKFENDAFNGGVDVTIDGNDGN 720
Db 721 DRLFGGKGDDIILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780
QY 721 DRLFGGKGDDIILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780
Db 781 FSDSNLKDITFEKVKNLVTITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEEIIIGQ 840
QY 781 FSDSNLKDITFEKVKNLVTITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEEIIIGQ 840
Db 841 NGERITTSKQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
QY 841 NGERITTSKQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSFTSSN 900
Db 901 DSRNVLVAPTSMLDQSLSSLOFARGS 926
QY 901 DSRNVLVAPTSMLDQSLSSLOFARGS 926

RESULT 9

ID US-08-878-748-6 STANDARD; PRG: 926 AA.

XX xxxxxx

Sequence 6, Application US/08878748

Sequence 6, Application US/08878748

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: REDMOND, MARK J.

APPLICANT: HUGHES, HUW P.A.

TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 635 BRYANT STREET

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/878,748

FILING DATE: 19-JUN-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,156

FILING DATE: 10-FEB-1995

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/779,171

FILING DATE: 16-OCT-1991

CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.21
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 926 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 926 AA; 99346 MW; 4207190 CN;

Query Match 98.6%; Score 6128; DB 12; Length 926;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKGTGAKKIILYIPQNYQYDTEQNGLQDLVKAABELGIEVQREERNIIATA 60

QY 1 MATVIDLSFPKGTGAKKIILYIPQNYQYDTEQNGLQDLVKAABELGIEVQREERNIIATA 60

Db 61 QTSLGTTIQTALGLTERGIVLSAPOIDKLLQKTGAQALGSAESIVONANKAKTVLSGIQS 120

QY 61 QTSLGTTIQTALGLTERGIVLSAPOIDKLLQKTGAQALGSAESIVONANKAKTVLSGIQS 120

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QY 241 NOVVGNTIKAVSSYTLAQRVAAGLSSTGTPVAALTAFTVSLAISPLAFAGIADKENHAKSL 300

Db 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASTVTAINTALAAIAGGVSAAAAGSVIASPIA 360

QY 301 ESYAERFKKLGVDGNLLAEYQRTGTTIDASTVTAINTALAAIAGGVSAAAAGSVIASPIA 360

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QY 361 LLVSGITGVISTILQYSKQAMFEHVANKIHNKIVWEKNNHGNKYNFENGYDARYLANIQD 420

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QY 421 NMKFLNLLNKELQAEVTAITQQQWDDNNIGDLGSLRGEKVLGSKAVYDFAPEGKHKA 480

Db 481 DKLVLQDSANGIIDVNSGKAKTOHILFRTPLLTGCTEHRERVQTKYEYITKLNINRVD 540

QY 481 DKLVLQDSANGIIDVNSGKAKTOHILFRTPLLTGCTEHRERVQTKYEYITKLNINRVD 540

Db 541 SWKITDGAASSTFDLTNNVQRIEGLDAGNAGVTCTKTKIIAKLGEEDNNVFGSGTTEI 600

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QY 721 DRLFGGKGDDIILDGGNGDDFIDGGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780

Db 781 FSDSNLKDITFEKVKNLVTITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEEIIIGQ 840

QY 781 FSDSNLKDITFEKVKNLVTITNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEEIIIGQ 840

QY 781 FSDSNLKDITFEKVKHNLVTNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 Db 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLSSVSATSSN 900
 QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLSSVSATSSN 900
 Db 901 DSRNLVAPTSMLDQSLSSLOFARG 926
 QY 901 DSRNLVAPTSMLDQSLSSLOFARG 926
 RESULT 10
 ID US-07-779-171-14 STANDARD; PRT: 926 AA.
 AC xxxxxx
 DT
 XX
 XX
 XX
 XX
 DE Sequence 14, Application US/07779171
 CC Sequence 14, Application US/07779171
 CC GENERAL INFORMATION:
 CC APPLICANT: Potter, Andrew A.
 CC APPLICANT: Redmond, Mark J.
 CC APPLICANT: Hughes, Huw P. A.
 CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING
 CC TITLE OF INVENTION: PASTEURELLA HEAMOLYTICA LEUKOTOXIN CHIMERAS
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Morrison & Foerster
 CC STREET: 545 Middlefield Road, Suite 200
 CC CITY: Menlo Park
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94025
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/779,171
 CC FILING DATE: 19911016
 CC CLASSIFICATION: 424
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Robins, Roberta L.
 CC REGISTRATION NUMBER: 33,208
 CC REFERENCE/DOCKET NUMBER: 29310-2001600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-327-7250
 CC TELEFAX: 415-327-2951
 CC TELEX: 706141
 CC INFORMATION FOR SEQ ID NO: 14:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 926 amino acids
 CC TYPE: AMINO ACID
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 926 AA; 99346 MW; 4207190 CN;
 Query Match 98.68; Score 6128; DB 3; Length 926;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MATVIDLSFPKTKAKKILYIPONYQYDTQGNGLQDLVKAABEELGIEVOREERNIATA 60
 QY 1 MATVIDLSFPKTKAKKILYIPONYQYDTQGNGLQDLVKAABEELGIEVOREERNIATA 60
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 QY 61 QTSGLGTQTAIGTERGIVLSAPQIDKLLQKTRAGQALGSAESIVQNAKAKTVLSGIQS 120
 Db 121 ILGSVLAGMDLDEALQNNQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180

QY 121 ILGSVLAGMDLDEALQNNQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180
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 QY 181 QNKGIGTIGDGLKNGTGGDLKAGLDVTSGLLSGATAALVLDKNAKSTAKKVGAGFELA 240
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 QY 301 ESYAERFKKLYGDDGNLLAEYQRTGTIDASVTAINATAAGGVSAAAAGSVIASPIA 360
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 QY 361 LLVSGITGVISTILOYSKOAMFEHVANKIHNKIVEKNNHGNKYNFENGIDARYLANLOD 420
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 QY 421 NMKFLNLNKLQAEKVIAITQQQWNNIGDLAGISRLGKVLGSKAYVDAFEEGKHKA 480
 Db 481 DKLVLQDSANGIDVNSGKAKTQHILFRTPLTPTGTEHRERVOTGKYEYITKLNINRVD 540
 QY 481 DKLVLQDSANGIDVNSGKAKTQHILFRTPLTPTGTEHRERVOTGKYEYITKLNINRVD 540
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 QY 541 SKMITDGAASFTDLTNVVRIGIELDNAGNVTKTETKIIAKLGEEDDNVFGSGTTEI 600
 Db 601 DGEYDVRVHYSRGNYGALTIDATKETECSYTVNRFVETGKALHEVTSTHTALVGNREE 660
 QY 601 DGEYDVRVHYSRGNYGALTIDATKETECSYTVNRFVETGKALHEVTSTHTALVGNREE 660
 Db 661 KTEYRHSNNQHHAGYTTKDTLKAVEREICTSHNDIFKSGKENDAFNGGVDGVDITDNGDN 720
 QY 661 KTEYRHSNNQHHAGYTTKDTLKAVEREICTSHNDIFKSGKENDAFNGGVDGVDITDNGDN 720
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 QY 721 DRLFGKGDDIILDGNGDDFIDGGKNDLLHGGKGDNDIFVHRKGDNDIITDSGDNDKLS 780
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 QY 781 FSDSNLKDITFEKVKHNLVTNSKKEKVTIQNWFEADFAKEVPNYKATKDEKIEIIGQ 840
 Db 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLSSVSATSSN 900
 QY 841 NGERITSKQVDDLIAGNGKITODELSKVVDNYELLKHSKNVTNSLDKLSSVSATSSN 900
 Db 901 DSRNLVAPTSMLDQSLSSLOFARG 926
 QY 901 DSRNLVAPTSMLDQSLSSLOFARG 926
 RESULT 11
 ID US-09-124-491-6 STANDARD; PRT: 926 AA.
 AC xxxxxx
 DT
 XX
 XX
 XX
 DE Sequence 6, Application US/09124491
 CC Sequence 6, Application US/09124491
 CC GENERAL INFORMATION:
 CC APPLICANT: POTTER, ANDREW A.
 CC APPLICANT: MANN, JOHN G.
 CC TITLE OF INVENTION: GORH-LEUKOTOXIN CHIMERAS
 CC NUMBER OF SEQUENCES: 34
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: REED & ROBINS LLP

CC STREET: 285 HAMILTON AVENUE, SUITE 200
CC CITY: PALO ALTO
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94301
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/124,491
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/694,865
CC FILING DATE: 09-AUG-1996
CC APPLICATION NUMBER: US 08/387,156
CC FILING DATE: 10-FEB-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/779,171
CC FILING DATE: 16-OCT-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: MCCracken, Thomas P.
CC REGISTRATION NUMBER: 38,548
CC REFERENCE/DOCKET NUMBER: 9001-0016.22
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415)327-3400
CC TELEFAX: (415)327-3231
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 926 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 926 AA: 99346 MW: 4207190 CN:
Query Match 98.6%; Score 6128; DB 15; Length 926;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MATVIDLSPKTKGAKKIIYIPONTQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
QY 1 MATVIDLSPKTKGAKKIIYIPONTQYDTEQNGQLDLVKAEEELGIEVQREERNIATA 60
Db 61 QTSIGTQTATGTERGIVLSAPOIDKLOKTKAGALGSASIVONANKAKTVLSGIQS 120
QY 61 QTSIGTQTATGTERGIVLSAPOIDKLOKTKAGALGSASIVONANKAKTVLSGIQS 120
Db 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELNSLIENIANSVKTLDFEGEIOISFGSKL 180
QY 121 ILGSLVAGMDLDEALQNNNSQHALAKAGLELNSLIENIANSVKTLDFEGEIOISFGSKL 180
Db 181 QNKGTLGLDKLNKIGGLDKAGLDVTSGLLSGATAALVLDKNAATKAKVAGFELA 240
QY 181 QNKGTLGLDKLNKIGGLDKAGLDVTSGLLSGATAALVLDKNAATKAKVAGFELA 240
Db 241 NOVGNITKAVSSYILAQRVAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
QY 241 NOVGNITKAVSSYILAQRVAGLSTGTPVAALIASTVSLAISPLAFAGIADKFNHAKSL 300
Db 301 ESYAERFKLGYDGNLLAEYORGTTIDASTVNTALAAAGGVSAAAAGSVIASPIA 360
QY 301 ESYAERFKLGYDGNLLAEYORGTTIDASTVNTALAAAGGVSAAAAGSVIASPIA 360
Db 361 LLVSGITGVISTILOYSKOAMEHVANKTHNKIVWEKNNHKNKFYNGDYDARYLANLQD 420
QY 361 LLVSGITGVISTILOYSKOAMEHVANKTHNKIVWEKNNHKNKFYNGDYDARYLANLQD 420
Db 421 NMKFLNKLQAEVIAITQQQDNNIGDLAISRUGEKVLGSKAYVDAAFEKGKHIKA 480

QY 421 NMKFLNKLQAEVIAITQQQDNNIGDLAISRUGEKVLGSKAYVDAAFEKGKHIKA 480
Db 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLTPGTEHRRVQTKYETIKLINRVD 540
QY 481 DKLVLQDSANGIIDVNSGKAKTQHILFRTPLTPGTEHRRVQTKYETIKLINRVD 540
Db 541 SWKITDGAASSTFDLTNVVQIRIGIELDNAGNVTKTKETIIAKLGEQDDNVFVSGTTEI 600
QY 541 SWKITDGAASSTFDLTNVVQIRIGIELDNAGNVTKTKETIIAKLGEQDDNVFVSGTTEI 600
Db 601 DGGEGYDRVHYSRGNYGALTIDATKETEQSGSYTVNRFVETGKALHEVTSHTALVGNREE 660
QY 601 DGGEGYDRVHYSRGNYGALTIDATKETEQSGSYTVNRFVETGKALHEVTSHTALVGNREE 660
Db 661 KIEYRHSNNQHAGYTKDTLKAVEEIIIGTSHNDIFKSGKFENDAFNGDGVDTIDGNDGN 720
QY 661 KIEYRHSNNQHAGYTKDTLKAVEEIIIGTSHNDIFKSGKFENDAFNGDGVDTIDGNDGN 720
Db 721 DRLFGGKGGDDILDGGNGDDFDGKGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780
QY 721 DRLFGGKGGDDILDGGNGDDFDGKGKNDLLHGGKGGDDIFVHRKGGDNDIITDSGNDKLS 780
Db 781 FSDSNLKDLPTEKVKHNLVITNSKKEVYTIQNWPREADFAKEVPNYKATKDEKIEEIIIG 840
QY 781 FSDSNLKDLPTEKVKHNLVITNSKKEVYTIQNWPREADFAKEVPNYKATKDEKIEEIIIG 840
Db 841 NGERITSQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900
QY 841 NGERITSQVDDLIAGKNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN 900
Db 901 DSRNVLVAPTSMLOQSLSLQFARGS 926
QY 901 DSRNVLVAPTSMLOQSLSLQFARGS 926
RESULT 12
ID US-08-455-970-10 STANDARD: PRT; 943 AA.
XX
AC xxxxxx
DT
DX
DE Sequence 10, Application US/08455970
CC Sequence 10, Application US/08455970
CC GENERAL INFORMATION:
CC APPLICANT: POTTER, ANDREW A.
CC APPLICANT: REDMOND, MARK J.
CC APPLICANT: HUGHES, HOW P.A.
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: REED & ROBINS
CC STREET: 285 HAMILTON AVENUE, SUITE 200
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: UNITED STATES OF AMERICA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/455,970
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC ATTORNEY/AGENT INFORMATION:

CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.10
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3400
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 943 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 943 AA: 101229 MW: 4397993 CN;

Db	841	NGERITSQVDDDLIAKNGKITODELSKVVDNYELLKHSKNVTNSLDKLISSVSAFTSSN	900
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Db	901	DSRNVLVAPTSMLDOSLSSLOFARGS	926
Qy	901	DSRNVLVAPTSMLDOSLSSLOFARGS	926
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XX	XXXXXX		
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DT			
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DE			
CC	Sequence 12, Application US/07779171		
CC	Sequence 12, Application US/07779171		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Potter, Andrew A.		
CC	APPLICANT: Redmond, Mark J.		
CC	APPLICANT: Hughes, Huw P.A.		
CC	TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING		
CC	TITLE OF INVENTION: PASTEURELLA HEAMOLYTICA LEUKOTOXIN CHIMERAS		
CC	NUMBER OF SEQUENCES: 14		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Morrison & Foerster		
CC	STREET: 545 Middlefield Road, Suite 200		
CC	CITY: Menlo Park		
CC	STATE: California		
CC	COUNTRY: USA		
CC	ZIP: 94025		

Qy	601	DGEGYDRVHSRNGYKALTDATKETEQGSYTVNRVETGKALHEVTSHTALVGNREE	660
Db	661	KIEYRHSNNQHHAGYTKDTLKAVEELIGTSHNDIEFKGSFNDAFNGGVDITDNGDN	720
Qy	661	KIEYRHSNNQHHAGYTKDTLKAVEELIGTSHNDIEFKGSFNDAFNGGVDITDNGDN	720
Db	721	DRLFGGKGDDILDGGNGDDPFDGGKGNLDLHGCKGDDIFVHRKGDGNDIITDSGDNKLS	780
Qy	721	DRLFGGKGDDILDGGNGDDPFDGGKGNLDLHGCKGDDIFVHRKGDGNDIITDSGDNKLS	780
Db	781	FSDSNLKDITFEVKVKNLVTNISKKEKVTIQNWFREADFAKEVPNTKATKDEKIEIIGQ	840
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Db 241 NOVVGNTIKAVSSYIIAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKENHAKSL 300
QY 241 NOVVGNTIKAVSSYIIAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKENHAKSL 300
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QY 301 ESYAERFKLGYDGNLLAEYQRTGTTIDASVTAINATAAGGVSAAAAGSVIASPTA 360
Db 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIVEWKNHGNKYNFENGVDARYLANLQD 420
QY 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIVEWKNHGNKYNFENGVDARYLANLQD 420
Db 421 NMKFLNLNKLQEAERVIAITQQQWNNNGDLAGISRLGKVLGSKAYVDFAFEGKHKA 480
QY 421 NMKFLNLNKLQEAERVIAITQQQWNNNGDLAGISRLGKVLGSKAYVDFAFEGKHKA 480
Db 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLLTGTEHRRVQTGKYEYITKLNINRVD 540
QY 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLLTGTEHRRVQTGKYEYITKLNINRVD 540
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QY 541 SWKITDGAASSTFDLTNVVQRIEGLDNDAGNVTKTKETKIIAKLGEGBDDNVFVSGTTEI 600
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QY 601 DGEQGYDRVHYSRNGYALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREE 660
Db 661 KIEYRHSNNQHHAGYYTKDTLKAVEREIICTSHNDIFKGSKFNDAGNGDGVDTIDGNDGN 720
QY 661 KIEYRHSNNQHHAGYYTKDTLKAVEREIICTSHNDIFKGSKFNDAGNGDGVDTIDGNDGN 720
Db 721 DRLFQGGKDDIILDGGNGDDFIDGGKGNLLHGGKGGDIFVHRKGGDNDIITDSGNDKLS 780
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Db 781 FSDSNLKDLTFFEKVHNLTITNSKKEKVITQNWFEADFAKEVPYKATKDEKIEEIQG 840
QY 781 FSDSNLKDLTFFEKVHNLTITNSKKEKVITQNWFEADFAKEVPYKATKDEKIEEIQG 840
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RESULT 14

ID US-07-779-171-8 STANDARD; PRT; 951 AA.

AC xxxxxx

Sequence 8, Application US/07779171

Sequence 8, Application US/07779171

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Hughes, Mark J.

APPLICANT: Hughes, Huw P.A.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING

TITLE OF INVENTION: PASTEURILLA HEAMOLYTICA LEUKOTOXIN CHIMERAS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

```
CC ADDRESSEE: Morrison & Foerster
CC STREET: 345 Middlefield Road, Suite 200
CC CITY: Menlo Park
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94025
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07779,171
CC FILING DATE: 19911016
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 29310-2001600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-327-7250
CC TELEFAX: 415-327-2951
CC TELEX: 706141
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 951 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 951 AA; 102128 MW; 4463354 CN;
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Query Match 98.6%; Score 6128; DB 3; Length 951;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MATVIDLSFPKTKAKKIILYIPQNYQYDTEQNGLQDLVKAEEELGIVQREERNIATA 60
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QY 61 QTSLGITQITAGLTERGIVLSAPOIDKLLQKTAKQALGSAESIVQNAKAKTVLSGIQS 120
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QY 121 ILGSLAGMDLDEALQNNQHALAKAGLELTNSLIENIANSVKTLDFEGEQISQFGSKL 180
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QY 361 LLVSGITGVISTILQYSKOAMFEHVANKIHNKIVEWKNHGNKYNFENGVDARYLANLQD 420
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Db 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLLTGTEHRRVQTGKYEYITKLNINRVD 540
QY 481 DKLVQDLSANGIIDVNSGKAKTOHILFRTPLLTGTEHRRVQTGKYEYITKLNINRVD 540
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QY 541 SWKITDGAASSTFDLTNVVQRIEGLDNDAGNVTKTKETKIIAKLGEGBDDNVFVSGTTEI 600
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QY 661 KIEYRHSNQHAGYYTQTLKAVEEIICTSHNDIFKSGKENDAFNGGVDITDGNNGN 720
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Db 901 DSRNLVAPTSMLDQSLSLQFARG 926
QY 901 DSRNLVAPTSMLDQSLSLQFARG 926

RESULT 15
ID US-08-455-970-14 STANDARD; PRT; 951 AA.
XX
AC
XX
DT

Sequence 14, Application US/08455970
Sequence 14, Application US/08455970
GENERAL INFORMATION:
CC APPLICANT: POTTER, ANDREW A.
CC APPLICANT: REDMOND, MARK J.
CC APPLICANT: HUGHES, HUW P.A.
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
CC TITLE OF INVENTION: CHIMERAS
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: REED & ROBINS
CC STREET: 285 HAMILTON AVENUE, SUITE 200
CC CITY: PALO ALTO
CC STATE: CALIFORNIA
CC COUNTRY: UNITED STATES OF AMERICA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/455,970
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/960,932
CC FILING DATE: 14-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: ROBINS, ROBERTA L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 9001-0016.10
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 327-3400
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 951 amino acids

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 951 AA; 102128 MW; 4463354 CN;
Query Match 98.6%; Score 6128; DB 8; Length 951;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MATVIDLSFPKTKGAKKIIILYIPQNYQYDTEQNGQLDVLKAAEELGIEVQREERNIIATA 60
QY 1 MATVIDLSFPKTKGAKKIIILYIPQNYQYDTEQNGQLDVLKAAEELGIEVQREERNIIATA 60
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QY 61 QTSLSGTIQTALIGLTERGIVLSAPQIDKLQKTAKOALGSAESIIVONANKAKTVLSGQS 120
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QY 361 LLVSGITGVISTILOYSKOAMPEHVANKIHKNKIVWEKNHGNKYNFENGVDARYLANLOD 420
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QY 481 DKLVLDSANGIIDVSNKSKAKTOHILFPTPLLTPTGTEHREVRVOTGKYEYITKLNINRVD 540
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QY 661 KIEYRHSNQHAGYYTQTLKAVEEIICTSHNDIFKSGKENDAFNGGVDITDGNNGN 720
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QY 781 FSDSNLKDITFEKVKHNLVITNSKKEKVITQNWFRADFAKEVPNYKATKDEKIEIIQ 840
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QY 841 NGERITSKQVDDLIAGNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISVSFAFTSSN 900
Db 901 DSRNLVAPTSMLDQSLSLQFARG 926
QY 901 DSRNLVAPTSMLDQSLSLQFARG 926

Search completed: Wed Dec 9 19:35:47 1998
Job time : 252 secs.

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